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GenCore version 5.1.6
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using sw model OM protein - protein search,

May 12, 2004, 11:11:35 ; Search time 21 Seconds (without alignments) 3041.484 Million cell updates/sec

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Run

US-10-087-217A-8 3475 1 MMTEKSNGVKSSPANNHNHH......NHEDDYLSDGINTPEPTAAE Title: Perfect score:

Sequence:

Scoring table:

283366 seqs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

alpha subunit of cyclic nucleotide-cyclic nucleotide-cyclic nucleotide-alpha subunit of r cGMP-gated ion cha cGMP-gated cation rod cyclic nucleot cGMP-gated cation olfactory cyclic nucleotide-cyclic nucleotidehypothetical prote potassium channel potassium channel potassium channel cyclic nucleotide-cyclic nucleotide-cAMP-gated channel Description SUMMARIES \$11517 \$35691 \$15691 \$150630 \$455251 \$74179 153197 148912 T17367 T33125 S32538 T20935 S74158 S74159 Query Match Length DB 44.8 44.8 45.2 45.2 46.2 46.2 46.2 46.2 46.2 46.2 46.3 61.2 559.5 558.8 558.6 57.4 4.4 3449 3231.5 3204.5 2219.5 Score Result No.

361 IGVLIFATIVGNVGSMISNMATRAEFQAKIDAVKHYMQFRKVSKDMEAKVIKWFDYLWT 420

IGVLIFATIVGNVGSMISNMNATRAEFQAKIDAVKHYMQFRKVSKDMEAKVIKWFDYLWT

361

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421

420

NKKTVDEREVLKNLPAKLRAEIAINVHLSTLKKVRIFQDWEAGLLVELVLKKRPQVFSPG 480

probable potassium	potassium channel	probable potassium	probable potassium	hypothetical prote	probable potassium	potassium channel	cyclic nucleotide-	potassium channel	potassium channel	probable potassium	potassium channel	probable calmoduli	hypothetical prote	cyclic nucleotide	potassium channel
13168	A40853	T31100	I38465	T19579	T31354	S55349	T51354	T04461	T42394	T07052	T52046	T04424	E86294	T10541	868699
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7	1174 2 A	~	1159 2	514 2	1017 2	688 2	716 2	662 2	934 2	845 2	828 2	702 2	738 2	698 2	787
1284 2	7	1087 2	•		•										
1284 2	11.6 1174 2	11.4 1087 2	•	11.0	10.9	10.9		10.3	10.2	10.1	10.0		9.8	9.7	7.6

ALIGNMENTS

	RESULT 1	
	811517	
	cyclic nucleotide-activated channel protein - rat	
	C; Species: Rattus norvegicus (Norway rat)	
	C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995	<pre>95 #text_change 13-Aug-1999</pre>
	100	
	Nature 247 104-107 1000	K.K.
	A:Title: Primary structure and functional expression of	sion of a cyclic nucleotide-activated c
	A; Reference number: S11517; MUID: 90370115; PMID: 1697649	
	A; Accession: S11517	
	A; Molecule type: mRNA	
	A) CASILLIAND AND VECETO. NITh. AECTION DITMICANNOTE 1. DITMICANOTE 1. DITMICANOTE 1. DITMICANOTE 1. DITMICANOTE 1. DITMICANOTE 1.	1. DID: CEC702
	C.Superfamily: cyclic nucleotide-gated channel; caMp receptor protein cyclic nucleotide	AMP receptor protein cyclic nucleotide
	C; Keywords: transmembrane protein	
	F;456-580/Domain: cAMP receptor protein cyclic nucleotide-binding	scleotide-binding domain homology <cap:< td=""></cap:<>
	99.3%;	3.2; Length 664;
	Best Local Similarity 99.5%; Freq. No. /.le-235 Matches 661; Conservative 0; Mismatches 3	.235; 3; Indels 0; Gaps 0;
•	Qy 1 MWTEKSNGVKSSPANNHNHHPPPSIKANGKDDHRAGSRPQSVAADDDTSPELQRLAEMDT	AGSRPOSVAADDDTSPELORIAEMDT 60
	Db 1 WYTEKSNGVKSSPANNHNHHPPPSIKANGKDDHRAGSRPQSVAADDDTSPELQRLAEWDT	
	Qy 61 PRRGRGGFQRIVRLVGVIRDWANKNFREEEPRPDSFLERFRGPELQIVITHQGDDKGGKD	SFLERFRGPELQTVTTHQGDDKGGKD 120
	TASSAME THE THE TASK A GAT TASK A	agraph and a second sec
	Tq	
	QY 121 GEGKGTKKKFELFVLDPAGDMYYRWLFVIAMPVLYNWCLLVARACFSDLQRNYFVVWLVL	KNWCLLVARACFSDLQRNYFVVWLVL 180
	DD 121 GEGKGIKKKFELFVLDPAGDMYYRWLFVIAMPVLYNWCLLVARACFSDLQRNYFVVWLVL	INWCLLVARACFSDLQRNYFVVWLVL 180
	Qy 181 DYFSDTVXIADLIRLRTGFLEQGLLVKDPKKLRDNYIHTLQFKLDVASIIPTDLIYFAV	ONYIHTLQFKLDVASIIPTDLIYFAV 240
	DS 181 DYPSDTVYIADLIIRLRTGFLEQGLLVKDPKKLRDNYIHTLGFKLDVASIIPTDLIYFAV	JIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
	Qy 241 GIHSPEVRELLHPARMFEFDRTETRISYDNIFRISNIVULYILVIIHWNACIYYVISK	FRISHLVLYILVIIHWNACIYYVISK 300
	Db 241 GIHSPEVRENRLIHFARMFEFFDRTETRISYPNIFRISNLVLYILVIHMNACIYYVISK	FRISNLVLYILVIIHWNACIYYVISK 300
	Qy 301 SIGEGVDTWVYPNITDPEYGYLAREYIYCLYWSTLTLTTGGTPPPVKDEEYLFVIFDFL	LILILIGEIPPVKDEEYLFVIFDFL 360
	Db 301 SIGFGVDTWVYPNITDPBYGYLAREYIYCLYWSTLTIATIGETPPPVKDEEYLFVIFDFL	
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421 NKKTY 481 DYICK 481 DYICK 541 NIRSI 601 BKLEC 601 BKLEC 601 BKLEC	Qy 482 YICRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSKMGNRRTAN 541 Db 548 YICRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSKMGNRRTAN 607 Qy 542 IRSLGYSDLFCLSKDDLMEAVTEADDAKKVLEERGREILMKGGLLDENEVAASMEVDVQE 601 Db 608 IRSLGYSDLFCLSKDDLMEAVTEYPDAKKVLEERGREILMKGGLLDENEVAASMEVDVQE 667 Qy 602 KLEQLETNWDTLYTRFAELLAEYTGAQQKLKQRITVLETKWKQNHEDDYLSDGINTPEPT 661 Db 668 KLKQLETNWETLYTRFGRLLAEYTGAQQKLKQRITVLETKWKQNHEDDYLSDGMNSPEPA 727 Qy 662 AAE 664 Db 728 AAE 730
661 TAAE 664 17 2 10 nucleotide-gated channel protein - rabbit ecies: Oryctolagus cuniculus (domestic rabbit) 18 13-3an-1995 #sequence_revision 13-Jan-1995 #text ecision: 335691 19 1	RESULT 3 Sl1521 CAMP-gated channel protein - bovine C;Species: Bos primigenius taurus (cattle) C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000 C;Accession: Sl1521 R;Ludwig, J.; Margalit, T.; Eismann, E.; Lancet, D.; Kaupp, U.B. FEBS Lett. 270, 24-29, 1990 A;Title: Primary structure of CAMP-gated channel from bovine olfactory epithe A;Reference number: Sl1521; MUID:91032022; PMID:1699793 A;Reference sl1521; MUID:91032022; PMID:1699793 A;References: Callon A;References: GBX55010; NID:9287743; PIDN:CAA38754.1; PID:9287744 A;Rocoule type: mRNA A;Residues: 1-663 -6100 A;Cross-references: GBX55010; NID:9287743; PIDN:CAA38754.1; PID:9287744 C;Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic F;454-578/Domain: CAMP receptor protein cyclic F;454-578/Domain cyclic CAMP receptor protein cyclic Minister CAMP receptor protein cyclic Minister CAMP receptor protein cyclic Minister CAMP receptor protein cyclic Mini
Query Match 93.0%; Score 3231.5; DB 2; Length 732; Best Local Similarity 93.8%; Pred. No. 1.7e-219; Matches 622; Conservative 16; Mismatches 24; Indels 1; Gaps Z WIEKSNGVKSSPANNHNHPPPPSIKANGKDDHAGSRPOSVAADDDTSPELQRIAEMDTP	Matches 610; Conservative 27; Mismatches 23; Indels 1; Gaps 2 MIEKSNGVKSSPANNHNHEPPPSIKANGKDDHRAGSRPOSVAADDDTSPELQRLAEMDTP 61
CY 62 RRCRGGFORIVELYGVIRDWANKUFREEEPPPDSFLERFRGPELGTVTTHQGDDKGGKDG 121 128 QQRRGGFFRIVILGOVIRDWANRIFREEEARPDSFLERFRGPELGTVTTQGDGKGDKG 121 22 128 GQRTKKEFELFVLDPAGDWYRRLFVIAMPULXNWCLLVARACFSDLQRNYFVVWLVDD 181 24 DGKGTKKKFELFVLDPAGDWYRRLFVIAMPULXNWCLLVARACFSDLQRNYFVVWLVDD 181 25 1	Db 60 QORĞĞFRRİARLVĞVLÄEMÄYRNFREEEPRPDSFLERFRGPELHTVTTQĞDĞKĞDKDĞ 119 QY 122 EGKGTKKKFELFVLDPAGDWYTRWLFYIAMPVLYNWCLLVARACFSDLQRNYFVVWLVLD 181 120 EGKGTKKKFELFVLDPAGDWYTRWLFLIALPVLYNWCLLVARACFSDLQRNYFVVWLVLD 181 QY 182 YFSDTVXIADLIIRLRTGFLEQGLLVKDPKKLRDNYIHTLQFKLDVASIIPTDLIYFAVG 241 DD 180 YVSDVVYIADLIFLRTGFLEQGLLVKDPKKLRDNYIHTMQFKLDVASIIPTDLIYFAVG 239
IHSPEVRENKLHFARMFEFFDRTETRTSYPNIFRISNLVILIVIIHMACIYYVISKS IHNPELRFRKLHFARMFEFFDRTETRTSYPNIFRISNLVILIVIIHMACIYYVISKS IHNPELRFRKLHFARMFEFDRTETRTSYPNIFRISNLVILIVIIHMACIYYVISKS IGFGVDTWYYPNITDPEYGYLAREYIYCLYWSTLTLTTIGETPPPVKDEEYLFVIFDFLI IGFGVDTWYYPNITDPEYGYLAREYIYCLYWSTLTLTTIGETPPPVKDEEYLFVIFDFLI IGFGVDTWYYPNITDPEYGYLAREYIYCLYWSTLTLTTIGETPPPVKDEEYLFVIFDFLI IGFGVDTWYYPNITDPEYGYLAREYIYCLYWSTLTLTTIGETPPPVKDEEYLFVIFDFLI IGFGVDTWYYPNITDPEYGYLAREYIYCLYWSTLTLTTIGETPPPVKDEEYLFVIFDFLI IGFGVDTWYYPNITDPEYGYLAREYIYCLYWGFRKVSKDMEAKVIKWFDYLWTN KKTYDEREVLKNLPAKLBAEIAINVHLSTLKKVRIFQDCEAGLLVELVLKLRPQYFSPGD	240 IHNPEVRENRILHERMFEFFDRIFTRSYPNIFILITHINGACIYYALSKS 302 IGGGVDTWYYPNITDPEYGYLAREYIYCLYWSTLITLTTIGETPPPYKDEEYLEVIFDFLI 300 IGFGVDTWYYPNITDPEYGYLAREYIYCLYWSTLITLTTIGETPPPYKDEEYLEVIFDFLI 362 GVLIFATIVGNVGSMISNMNATRAEFQAKIDAVKHYMQFRKVSKDMEAKVIKMFDYLWTN 360 GVLIFATIVGNVGSMISNMNATRAEFQAKIDAVKHYMQFRKVSKDMEAKVIKMFDYLWTN 422 KKTVDEREVLKNLPAKLRAEIAINVHLSTLKKVRIFQDWEAGLLVELVLKLRPQVFSPGD 420 KKSVDEREVLKNLPAKLRAEIAINVHLSTLKKKVRIFQDWEAGLLVELVLKLRPQVFSPGD 420 KKSVDEREVLKNLPAKLRAEIAINVHLSTLKKKVRIFQDCEAGLLVELVLKLRPQVFSPGD 421 KKSVDEREVLKNLPAKLRAEIAINVHLSTLKKKVRIFQDCEAGLLVELVLKLRPQVFSPGD 422 KKSVDEREVLKNLPAKLRAEIAINVHLSTLKKKVRIFQDCEAGLLVELVLKLRPQVFSPGD 423 KTCRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSKMGNRRTAN 482 YICRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSKMGNRRTAN

Db 480 YICRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSKMGNRRTAN 539	Oy 475 OVFSPGDYICRKGDIGKEMYIIKEGKLAVVADDGYTQYALLSAGSCFGELSILNIKGSKM 534
Kaupp, U.E d channels	SULT 5 5251 clic nucleotide-gate clic nucleotide-gate Date: 06-Feb-1995 # Accession: A25251; Biel, M.; Zong, X.; Biel, M.; Zong, X.; Title: Another membe Reference number: A55251 Accession: A55251 Status: nucleic acid Sclatus: nucleic acid
ic nucleotide- omology «CAP»	A; Mostcute Lype: Intura A; Residues: 1-706 (SEES) A; Cross-references: GB:X76485; NID:g488728; PIDN:CAAS4023.1; PID:g488729 A; Experimental source: Kidney R; Weyand, I:, Godde, M; Frings, S.; Weiner, J.; Mueller, F.; Altenhofen, W.; Hatt, H.; Nature 368, 859-863, 1994 A; Title: Cloning and functional expression of a cyclic-nucleotide-gated channel from ma
QY 16 NHNHHPPPSIKANGKDDHRAGSRPQSVAADDDTSPELQRLAEND 59	A; Reference number: 5439/b; Mull:94241295; FMID:/512693 A; Accession: 94376 A; Accession: Janoer: 543776 A; Status: preliminary; nucleic acid sequence not shown A; Molecule type: mRNA A; Residues: 1-706 < WRX> A; Cross-references: GB:X89600; NID:g908823; PIDN:CAA61759.1; PID:g908824 C; Genetics:
Qy 114D 114 Db 123 GIREQPGGVNGPWFLARFNVNFSNNTNBDKKEEKKEVKEEKKEEKKEEKKEEKKEEKKDKKDDKKDD 182	A; Gene: CNG3 C; Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide C; Keywords: cGMP binding; ion channel; ion transport; membrane protein F;501-625/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <cap></cap>
QY 115 DKGGKDGEGKGTKKKEELFVLDPAGDWYYRMLFVIAMPVLYNWCLLVARACFSDLGRNYF 174 : : : :	Query Match 61.6%; Score 2140; DB 2; Length 706; Best Local Similarity 60.4%; Pred. No. 1.1e-142; Matches 419; Conservative 94; Mismatches 119; Indels 62; Gaps 7;
QY 175 VVWLVLDYFSDTVYIADLIIRLRTGFLEQGLLVKDFKKLRDNYIHTLQFKLDVASIIPTD 234	QY 11 SSPANNHNHPPPSIKANGKD-DHRAGSRPQSVAADDDTSPELQRLAEMDTPRRGRG 66
Oy 235 LIYFAVGIHSPEVRRILHFARMEEFFDRIETRISYPNIFRISNLVLYILVIIHMNACI 294	QY 67GFQRIVRLVGVIRDWANKNFREEEPRPDSFLERFRGPELQTVTTHQG 113 Db 62 QSSFTSQGPTRLSRLISLRAWSARHLHQEDQRPDSFLERFRGAELQEVSSRESHVQFNV 121
OY 295 YYVISKSIGFCVDTWVYPNITDPEVCYLAREYIYCLYWSTLTLTTIGETBPPVKDEEYLF 354	Qy 114GKGTKKKFELFVLD 136 Db 122 GSQEPPDRGRSAWPLARNNTNTCNNSEKDDKAKKEEKKEEKKENPKKEEKKKDSVVMD 181
Qy 355 VIEDELIGVLIFATIVGNVGSMISNMNATRAEFQAKIDAVKHYNGFRKVSKDMEAKVIKW 414	QY 137 PAGDWYYRWLFVIAMPVLYNWCLIVARACFSDLQRNYFVWLVLDYFSDTVYIADLIIRL 196 ::
OY 415 FDYLWINKKTVDEREVLKNLPAKLRAEIAINVHLSTLKKVRIFODWEAGLLVELVLKLRP 474	OY 197 RIGELEGGLLVKDPKKLRDNYIHTLQFKLDVASIIPTDLIYFAVGIHSPEVRFNRLLHFA 256

257 RMFEFFDRTETRISYPNIFRISNLVLYILVIIHWNACIYYVISKSIGFGVDTWYYPNITD 302 RIFEFFDRTETRINYPNMFRIGNLVLYILLIIHWNACIYFAISKFIGFGTDSWYYPNYSN 317 PEYGYLAREYIYCLYWSTLTLTTIGETPPPYKDEEXLEVIFDELIGYLIFAITYGNVGSM 31862 PEYGKLSRKYIYSLWSTLTLTTIGETPPPYKDEEXLEVIIDFLYGYLIFAITYGNVGSM 377 ISNNNATRAEFQAKIDAVKHYNQFRKYSKDMEAKVIKMPDYLMTNKKTYDEREVLKNLPA 422 ISNNNATRAEFQAKIDSIKOYNOFRKYTKDLETVIRMPDYLMANKKTYDEREVLKNLPA 422 ISNNNASRAEFQAKIDSIKOYNOFRKYTKDLETVIRMPDYLMANKKTYDEREVLKNLPA 423 ISNNNASRAEFQAKIDSIKOYNOFRKYTKDLETRVIRMPDYLMANKKTYDEREVLKSLED		LLVKOPKKLRDNYIHTLOFKLDVASIIPTDLIYFAVGIHSPEVRFNRLLHFARMFEFFDR
OY 437 KLARALIAINHLESTLKKVNRIRODMEAGLIVELVIKKURPOVESRGIGKEMYII 496 Db 482 KLKARIAINVHLDTLRKVRIRODCEAGLIVELVIKLRPAVFSRGDYICKKGDIGKEMYII 496 OY 497 KEGKLAVVADDGVTQYALLSAGSCFGRIILNIKGSKMGNRITANIRSLGYSDLFCLSKD 556	Oy 385 Db 376 Oy 445 Db 436	S AEGGRIDAGHYMGERKUSEOMEAKUIKMEDYLMYKKTUDEREJLKARABIAI 444
QY 557 DIMBAVTBARDAKKVLEERGREILMKWGLLDENEVAASME-VDVQEKLEQLETNMDTLYT 615 DD 602 DLMEALTEYPEAKKALEEKGRQILMKDNLIDEELAKAGADPKDIEEKVEHLETSLDSLQT 661 QY 616 RFARLLAEYTGAQQKLKQRITVLETKWKQNHEDD 649 DD 662 RFARLLAEYNAQKLKQRITVLETKWKQNHEDD 649 DD 662 RFARLLAEYNATQMKVKQRLSQLESQVKMGLPPD 695	Qy 505 Db 496 Qy 565 Db 556	ADDGVTQYALLSAGSCFGEISILAIKGSKWGNRRTAANIRSLGYSDIFCLSKDDLMEAVTB 564
RESULT 6 JH0560 cyclic nucleotide-gated channel - channel catfish C;Species: Ictalurus punctatus (channel catfish) C;Date: 10-8ep-1999 #sequence revision 10-8ep-1999 #text change 10-8ep-1999	Qy 624 Db 616 RESULT 7	4 YIGAQQKLKORITVLETKM 642
., R.; Siegelbaum, S.A.; Chess: the cyclic nucleotide-gated	S74179 S74179 Cyclic nucle Cyslic nucle Cyslic 14-A C,Date: 14-A C,Accession: R,YU, W.P. ', FEBS Lett. ', FEBS Lett. 'A A,Title: Mol A,Reference A,Accession:	S74179 cyclic nucleotide-gated channel protein - human cyclic nucleotide gated channel protein - human c;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 16-Jul-1999 C;Accession: S74179 R;Yu, W.P.; Grunwald, M.E.; Yau, K.W. FEBS Lett. 393, 211-215, 1996 A;Title: Molecular cloning, functional expression and chromosomal localization of a hum A;Reference mumber: S74179; MUID:96409310; PMID:8814292 A;Accession: S74179
A; Experimental source: olfactory epithelium C; Comment: This cyclic nucleotide-gated channel is activated equally well by both CAMP a C; Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide- C; Superfamily: cxolic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide- C; Keywords: cAMP binding; cGMP binding; ion channel; ion transport; olfaction; transmembrane #status predicted <ts1- #status="" <ts2-="" <ts3-="" <ts3-<="" domain:="" f;173-153="" f;241-261="" f;271-236="" f;271-275="" f;271-277="" predicted="" td="" transmembrane=""><td>A,Status: no A,Molecule t A,Residues: A,Experiment C,Genetics: A,Map positi C,Superfamil C,Keywords: F;482-607/Do</td><td>t compared with conceptual translation ype: mRNA al source: retina on: 2 y: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide ion channel; ion transport; membrane protein main: cAMP receptor protein cyclic nucleotide.</td></ts1->	A,Status: no A,Molecule t A,Residues: A,Experiment C,Genetics: A,Map positi C,Superfamil C,Keywords: F;482-607/Do	t compared with conceptual translation ype: mRNA al source: retina on: 2 y: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide ion channel; ion transport; membrane protein main: cAMP receptor protein cyclic nucleotide.
oinding domain homology <cap></cap>	Query Matc Best Local Matches 4	Query Match 61.2%; Score 2126.5; DB 2; Length 695; Best Local Similarity 61.5%; Pred. No. 9.9e-142; Matches 429; Conservative 92; Mismatches 130; Indels 47; Gaps 11;
Best Local Similarity 67.7%; Pred. No. 4.6e-142; Matches 419; Conservative 68; Mismatches 110; Indels 34 RAGSRPQSVAADDDTSPELQRLAEMDTPRRGRGGPQRIVR	\$ 6 \$ \$ \$	S KSNGVKSSPANNHNHPPPSIKANGKDDHRAGSRPQSVAADDDTSPELQRLAEMDT- 60
OY 87 REBERPLEDSFLERFROPELQIVITHQGDDKGGKDGEGKGTKKKFELFVLDPAGDWYK 144	Qy 114 Db 116 Qy 149	
14. MEFFIALASDINWIMDVARACFDQLQDDBNFFLWVGLDYILLDDYCIRLRIGYLEQXF	Db 175	: : : :

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CGMP-gated ion channel protein - bovine
CGMP-gated ion channel protein - bovine
CGMP-gated ion channel protein - bovine
CGMP-gated Sprimigenius taurus (cattle)
CC;Species: Bos primigenius taurus (cattle)
C;Accession: 807103
R;Kaupp, U.B.; Niidome, T.; Tanabe, T.; Terada, S.; Boenigk, W.; Stuehmer, W.; Cook, N.
Nature 342, 762-766, 1989
A;Title: Primary structure and functional expression from complementary DNA of the rod
A;Reference number: S07103; MUID:90098076; PMID:2481236
A;Residues: 1000
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-690 - KKAD-
A;Residues: 1-690 - KKAD-
A;Cross-references: GB:X51604; NID:g203; PIDN:CAA55947.1; PID:g204
A;Note: part of this sequence was confirmed by protein sequencing
C;Keywords: cGNP binding; eye; ion channel; cAMP receptor protein cyclic nucleotide
C;Keywords: cGNP binding; eye; ion channel; no transport; retina; transmembrane protein
F;477-601/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP:
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                                                                              WVYPNITDPEYGYLAREYIYCLYWSTLTLTTIGETPPPVKDEEYLFVIFDFLIGVLIFAT
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Best Local Similarity 63.5%; Pred. No. 6.3e-136;
Matches 401; Conservative 82; Mismatches 118;
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150680
alpha subunit of rod photoreceptor CNG-channel - chicken
c;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Aug-1999
C;Accession: 150680
R;Bonigk, W; Altenhofen, W; Muller, F.; Dose, A.; Illing, M.; Molday, R.S.; Kaupp, U.B.
R;Bonigk, W; Altenhofen, W; Muller, F.; Dose, A.; Illing, M.; Molday, R.S.; Kaupp, U.B.
R;Bonigk, W; Altenhofen, W; Muller, F.; Dose, A.; Illing, M.; Molday, R.S.; Kaupp, U.B.
R;Bonigk, W; Altenhofen, W; Muller, F.; Dose, A.; Illing, M.; Molday, R.S.; Kaupp, U.B.
A;Reference number: 150680
A;Reference number: 150680
A;Reference number: 150680
A;Residus: preliminary; translated from GB/EMBL/DDBJ
A;Rosidus: 1-645 cBON-A;Roside GB/EMBL/DDBJ
A;Rosidus: 1-645 cBON-A;Roside-gated channel; cAMP receptor protein cyclic nucleotide-F;811-555/Domain: cAMP receptor protein cyclic nucleotide-F;431-555/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology cGAP>
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                          DPKKLRDNY1HTLQFKLDVAS11PTDL1YFAVG1HSPEVRFNRLLHFARMFEFFDRTETR
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62.9%; Pred. No. 1.4e-137;
live 78; Mismatches 123;
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Cipate: 03-May-1994 #sequence_revision 03-May-1994 #text_change 13-Aug-1999
Cipate: Distinct 267, 6257-6262, 1992
Airitle: Primary structure and chromosomal localization of human and mouse rod photorec Aireference number: A42161; MUD:92210603; PMID:1372902
Airitle: Primary

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A44842

GGMP-gated ion channel protein - human

N;Alternate names: rod photoreceptor GGMP-gated channel
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Date: 12: 3248-3256, 1992
A;Telte: Human rod photoreceptor GMP-gated channel: amino acid sequence, gene structure
A;Reference number: A44842
A;Reference number: A44842
A;Rocasidues: 1-686 AcDHA>
A;Rocasidues: 1-686 AcDHA>
A;Rossidues: retina
A;Rocas-references: GB:342457; NID:g252853; PIDN:AAB22778.1; PID:g252854
A;Experimental source: retina
A;Roct: sequence extracted from NCBI backbone (NCBIN:110250, NCBIP:110251)
A;Roct: intron positions were determined from genomic sequence
C;Genetics:
A;Genetics:
A;Geneti
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IK 413 413 436 496 496 496 496 4 592 652 652	Db 438 DYLWTDKKTVDEKEVLKYLPDKLRABIAINVHLDTLKKVRIFADCEAGLLVELVLKLQPQ 497 QY 476 VFSFGDYICRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSKMG 535
676 one of the service of the servi	CGMP-gated cation channel, rod photoreceptor - mouse CjSpecies: Mus musculus (house mouse) CjSpecies: Mus musculus (house mouse) CjSpecies: Mus musculus (house mouse) CjAccession: B42161 R,Ppittler, S.J.; Lee, A.K.; Altherr, M.R.; Howard, T.A.; Seldin, M.F.; Hurwitz, R.L.; P. J. Biol. Chem. 267, 6257-6262, 1992 A,Title: Primary structure and chromosomal localization of human and mouse rod photorec A; Reference number: A42161; MUID:92210603; PMID:1372902 A,Title: Primary structure and chromosomal localization of human and mouse rod photorec A; Reference number: A42161 A,Reference number: A42161 A,Reference number: A42161 A,Reference number: A62161 A,Status: preliminary A,Reference number: A62161 A,Status: preliminary A,Residues: 1-688 roll. A;Cross-references: GB:M84742 A;Note: authors translated the codon TAT for residue 544 as Thr C;Superfamily: cyclic nucleotide-gated channel; CAMP receptor protein cyclic nucleotide C;Keywords: CGMP binding F;475-599/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <cap: 1.6e-132;="" 143;="" 23;="" 398;="" 61.0%;="" 6;<="" 88;="" best="" conservative="" gaps="" indels="" local="" match="" matches="" mismatches="" no.="" pred.="" query="" similarity="" td=""></cap:>
Query Match 58.1%; Score 2017.5; DB 2; Length 691; Best Local Similarity 61.3%; Pred. No. 4.6e-134; Matches 398; Conservative 94; Mismatches 126; Indels 31; Gaps 7; Qy 23 PSIKANGKODHRAGSRROGYWAADDDTSPELQRLAREMOTIPRRGRGGFQR 70 Db 21 PDIEKEIRRWENGARSSFSDDGGDDDSASMFEESENETPHARDSCRNNSQRRDFSQR 77	QY 21 PPPSIKANGKDDHRAGSRPQSVAADDDTSPELQRLAEMDTPRRGRGGFQRIVRLV 75 Db 20 PNVIVPALEKEIRRMENGACSSFSDDDNGSLSEESENEDSFFRSNSYKRRGPSQREQHLP 79 QY 76 GVIRDWANKNFREEEPRPDSFLERPRGPELQTVTTHQGDDKGGK 119 Db 80 GTWALFNVNNSSNKDQEPKEKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
OY 71 IVRLVGVIRDWANKANFREEBRRPDSFLERFRGPELQTVTTHQGDDKG 117 DD 78 EQYLPGAIALFNVANSSNKEQEPKEKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	QY 120 DGBGKGTKKKFELFVLDPAGDWYYRWLFVIAMPULYNWCLLVARACFSDLQRNYFVVWLV 179 Db 140 TKEKKEBEKK-EVVVIDPSGNTYYNWLFCITLPVMYNWTMIIARACFDELQSDYLEYWLI 198 QY 180 LDYFSDTVXIADLIIRLRYGFLEQGLLVKDPKKKLRDNYIHTLQFKLDVASIIPTDLIYFA 239 Db 199 FDYVSNVYYLADMFKTRTGYLEQGLLVKDRWKLIEKYKANLQFKLDVLSVIPTDLIYIK 258
OY 176 VMLVLDYFSDTVYIADLIIRLRTGFLEQGLLVKDPKKLRDNYIHTLQPKLDVASIIPTDL 235 :	OY 240 VGIHSPEVRENRLLHPARMFEFFDRTETRTSYPNIFRISNLVLYILVIIHWNACIYYVIS 299
Cy 296 YVISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWSTLTLTTIGETPPPVKDEEYLFV 355 :	LIGVLIFATIVGNVGSMISNNNATRAEFQAKIDAVKHYMQFRKVSKOMEAKVIKWFDYLM LIGVLIFATIVGNIGSMISNNNAARAEFQSRVDAIKOMNFRNVSKOMEKRVIKWFDYLM LLIGVLIFATIVGNIGSMISNNNAARAEFQSRVDAIKOMNFRNVSKOMEKRVIKMFDYLM TNKKTVDEREVLKNLPAKLRAEIAINVHLSTLKKVRIFODWEAGLLVELVLKLRPOVFSP [

	Db 438 GYSDLFCLSKEDLREVLSEYPQAQAVMEEKGREILLKMNKLDVNAEAAEIALQEATES 495 QY 602 KLEQLETNMDTLYTRFARLLAEYTGAQOKLKQRITVLETKMKQNHEDDYLSDGINTPEP 660
OY 599 VQEKLEQLETNMDTLYTRFARLLAEYTGAQQKLKQRITVLETKWKQNHEDDY 650 	orosophila sp.)
RESULT 14 159327 Olfactory cyclic nuclectide gated cation channel - rat C;Species: Rattus norvegicus (Norway rat) C;Species: Rattus norvegicus (Norway rat) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 31-Mar-2000 C;Accession: 159327, 158165 R;Bradley, J.; Li, J.; Davidson, N.; Lester, H.A.; Zinn, K. Proc. Natl. Acad. Sci. U.S.A. 91, 88990-8894, 1994 A;Title: Heteromeric Olfactory cyclic nucleotide-gated channels: A new subunit that conf A;Reference number: 159327; MUID:94377458; PMID:952325	C;Date: C;Access R;Bauman R;Bauman EMBO J: A;Tille: A;Access A;Status A;Molecu C;Geneti
	A;Gene: FlyBase:Cng A;Cross-references: FlyBase:FBgn0014462 C;Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide F;429-553/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <cap></cap>
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A;Accession: 158165 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNP A;Residues: 1-575 < RR2>	QY 87 REBEPRPDSFLERFRGPELQTVTTHQGDDKGGKDGECKGTKKKFELFVLDPA 138
A;Cross-references: EMBL:U12425; NID:9548083; PIDN:AAA64748.1; PID:9548084 C;Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide F;348-472/Domain: CAMP receptor protein cyclic nucleotide-binding domain homology <capp< td=""><td>QY 139 GDWYXRWLFVIAMPULYNWCLLVARACFSDLQRNYFVVMLVLDYFSDTVYIADLIIRLRT 198 104 LQSHYRWLAIVSLAVLYNIIFVVGRAVFWEINKSAPAFWYLLDYLCDFIYLLDTLVHMHE 163</td></capp<>	QY 139 GDWYXRWLFVIAMPULYNWCLLVARACFSDLQRNYFVVMLVLDYFSDTVYIADLIIRLRT 198 104 LQSHYRWLAIVSLAVLYNIIFVVGRAVFWEINKSAPAFWYLLDYLCDFIYLLDTLVHMHE 163
Query Match 43.7%; Score 1518; DB 2; Length 575; Best Local Similarity 53.8%; Pred. No. 5.3e-99; Matches 290; Conservative 101; Mismatches 142; Indels 6; Gaps 2;	QY 199 GFLEQGLLVKDPKKLRDNYIHTLGFKLDVASIIPTDLIYFAVGIHSPEVRF 249
QY 126 TKKKFELFVLDPAGDWYXRWLFVIAMPVLYNWCLLVARACFSDLQRNYFVVWLVLDYFSD 185	QY 250 NRLLHFARMFEFFDRTETRISYPNIFRISNLVLYILVIIHWNACIYYVISKSIGFGVDTW 309
Qy 186 TVXIADLIIRLRTGFLEQGLLVKDPKKLRDNYIHTLQFKLDVASIIPTDLIYFAVGIHSP 245	QY 310 VYPNITDPEXGYLARBYIYCLYWSTLTLTTTGETPPPVKDEKLFUFDFLIGVLIFATI 369
OY 246 EVRENRLIHFARMEEFFDRIETRISVENIFRISNLVIZILVIIHMNACIYYVISKSIGFG 305 	QY 370 VGNVGSMISNMNATRAEFQAKIDAVKHYMQFRKVSKDMEAKVIKWFDYLWTUKKTVDERE 429
QY 306 VDIWVYPNIIDPEYGYLAREYIYCLYWSTLTLTTIGETPPPVKDEEYLFVIFDFLIGVLI 365 :	QY 430 VLKNLPAKLRABIAINVHLSTLKKVRIFQDWEAGLLVELVLKLRPQVFSPGDYICRKGDI 489
QY 366 FATIVGNVGSMISNNNATRAEFQAKIDAVKHYMQFRKVSKDMBAKVIKWFDYLWTNKKTV 425	QY 490 GKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSKWGNRRTANIRSLGYSD 549
OY 426 DEREVLKNLPAKLRAEIAINVHLSTLKKVRIFQDWEAGLLVELVLKLRPQVFSFGDYICR 485 1	QY 550 LFCLSKDDLMBAVTEAPDAKKVLEBRGREILMKMGLLDENBVAASMEVDVQEKLEQLE 607
QY 486 KGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSKMGNRRTANIRSL 545	QY 608 THMDTLYTRFARLLAEYTGAQOKLKORITVLE 639 1::
QY 546 GYSDLFCLSKDDLMEAVTEAPDAKKVLEERGREILMKWGLLDENEVAASMEVDVQE 601	Search completed: May 12, 2004, 11:15:45

Job time : 23 secs

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Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2004
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protein search, using sw model OM protein May 12, 2004, 11:07:14 ; Search time 60 Seconds (without alignments) 3126.859 Million cell updates/sec Run on:

3475 1 MMTEKSNGVKSSPANNHNHH......NHEDDYLSDGINTPEPTAAE 664 US-10-087-217A-8 Title: Perfect score:

Sequence:

BLOSUM62

Scoring table:

1586107 seqs, 282547505 residues

Gapop 10.0 , Gapext 0.5

Searched:

1586107 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* A Geneseq 29Jan04:* 1: geneseqp1980s:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

Res

Description	Aae37222 Rat CNG c	Aae37221 Rat CNG c	Aae37224 Rat CNG c	Aae37220 Rat CNG c	Aae37223 Rat CNG c	Aag79529 Rat HBMYC	Aae37219 Rat CNG c	Aag79528 Mouse HBM	Aag79526 Rabbit HB	Aag79527 Cow HBMYC		Abg74914 Bovine CN	Abg74913 Bovine CN	Aae04894 Human tra	Abb78066 Amino aci	Abg72530 Novel hum	Novel	6	Abp98475 Amino aci	Aag79525 Variant H	Aag79524 HBMYCNG.	Aae15987 Human CNG	Aae38591 Human CNG	640	Add93244 Cyclic nu
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ALIGNMENTS

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AAE37222 standard; protein; 664 AA.
RESULT 1
                   AAE37222
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(first entry) 07-AUG-2003 AAE37222;

Rat CNG channel alpha subunit mutant (C460W+Y565A+E583M).

Rat; G protein-coupled receptor; cyclic nucleotide-gated channel; GPCR; cyclic nucleotide-gated channel; CNG channel; mutant; mutein.

Rattus norvegicus. Synthetic.

/note= "Wild type Cys substituted with Trp" Key Location/Qualifiers Misc-difference 460 Misc-difference 565

substituted with Ala" 583 /note= "Wild type Glu substituted with Met" 'note= "Wild type Tyr Misc-difference

WO2003038039-A2.

08-MAY-2003.

25-OCT-2002; 2002WO-US034122.

26-OCT-2001; 2001US-0330663P. 04-MAR-2002; 2002US-00087217.

(APTU-) APTUS PHARM INC.

Cao L; Yao Y, WPI; 2003-430510/40. N-PSDB; AAD56242.

New host cell comprising first and second nucleic acids with promoters that encode exogenous G protein-coupled receptor and cyclic nucleotidegated channel, respectively, useful for identifying agents that modulate GPCR activity.

Claim 13; Page 95-98; 98pp; English.

Ö The invention relates to compositions and methods for identifying

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protein-coupled receptor (GPCR), ligands and compounds that modulate GPCR -mediated activities. The invention also provides an host cell comprising first and second nucleic acids with promoters that encode exogenous G protein-coupled receptor and cyclic nucleotide-gated (CNG) channel respectively. The host cells are useful for identifying agents that modulate an activity mediated by a GPCR. The present sequence is rat CNG
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channel alpha subunit mutant.

CNG

Rat

(first entry)

07-AUG-2003

XEXEXEX

AAE37221;

664 AA

AAE37221 standard; protein;

AAE37221 ID AAE

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 protein-coupled receptor; cyclic nucleotide-gated channel; GPCR; nucleotide-gated channel; CNG channel; mutant; mutein.
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Pred. No. 0;
0; Mismatches
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04-MAR-2002; 2002US-00087217.
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Best Local Similarity 99.8%;
Matches 663; Conservative
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61 PRRGRGGFQRIVRLVGVIRDWANKNFREEBPRPDSFLERFRGPELQTVITHQGDDKGGKD 120
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      page 78-80 of
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                                                                                                      Length 664;
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                                                                                                      Score 3456; DB Pred. No. 0; 0; Mismatches
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    as SEQ ID
                                                                                                      Query Match
Best Local Similarity 99.7%;
Matches 662; Conservative
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      type protein shown specification
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Synthetic.
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                                                                                     DYICRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSKMGNRRTA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Wild type Cys substituted with His"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat CNG channel alpha subunit mutant (C460H+E583M)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
460
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE37224 standard; protein; 664 AA.
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Misc-difference
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421 NKKIVDEREVLKNLPAKLRAEIAINVHLSTLKKVRIFQDCEAGLLVELVLKLRPQVFSPG 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 channel; GPCR;
                                                                                                                                  DYICRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSKMGNRRTA
                                                                                                            NIRSLGYSDLFCLSKDDLMEAVTEAPDAKKVLEERGREILMKMGLLDENEVAASMEVDVQ
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cyclic nucleotide-gated channel; CNG channel; mutant; mutein
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04-MAR-2002; 2002US-00087217.
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                                                 /note= "Wild type Tyr substituted with Ala"
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Pred. No. 0;
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           Key Location/Qualifiers
Misc-difference 565
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04-MAR-2002; 2002US-00087217.
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Best Local Similarity 99.7
Matches 662; Conservative
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                                                                                                                                           PREGREGEGRIVALVGVIRDWANKNFREEEPRPDSFLERFRGPELQTVTTHQGDDKGGKD
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Pred. No. 0;
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Best Local Similarity
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                     Sequence 664 AA;
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GEGKGTKKKFELFVLDPAGDWYYRWLFVIAMPVLYNWCLLVARACFSDLQRNYFVVWLVL DYFSDTVXIADLIIRLRIGFLEQGLLVKDPKKLRDNYIHTLQFKLDVASIIPTDLIYFAV

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DYPSDTVYIADLIIRLRIGFLEGGLLVKDPKKLRDNYIHTLGFKLDVASIIPTDLIYFAV

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241 GIHSPEVRENRLÄHFARMFEFFDRIETRISYPNIFRISNLVLYILVIIHWNACIYYVISK

SIGFGVDTWVYPNITDPEYGYLAREYIYCLYWSTLTLTLTTIGETPPPVKDEEYLFVIFDFL SIGEGVOTWVYPNITOPEYGYLAREYIYCLYWSTLTLTIGETPPPVKDEEYLFVIFDFL IGVLIFATIVGNVGSMISNMNATRAEFQAKIDAVKHYMQFRKVSKDMEAKVIKWFDYLWT

301 301 NKKTVDEREVLKNLPAKLRAEIAINVHLSTLKKVRIFQDWEAGLLVELVLKLRPQVFSPG NKKTYDEREVIKNI.PAKLRAEIAINVHLSTLKKVRIFQDCEAGILVELVLVKRRPQVFSPG DYICRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSKMGNRRTA DYICKKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSKMGNRRTA

481

IGVLIFATIVGNVGSMISNMNATRAEFQAKIDAVKHYMQFRKVSKDMEAKVIKWFDYLWT

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361 421 421 481

GIHSPEVRFNRLLHFARMFEFFDRTETRTSYPNIFRISNLVLYILVIIHWNACIYYVISK

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New human HBMYCNG genes, useful for treating ion channel-related
disorders e.g. stroke, anxiety and depression, Alzheimer's or Parkinson's
disease, diabetes or arrhythmia.
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Best Local Similarity 99.5%; Pred. No. 0;
Matches 661; Conservative 0; Mismatche
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Rattus norvegicus.
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                     GEGKGTKKKFELFVLDPAGDWYYRWLFVIAMPVLYNWCLLVARACFSDLQRNYFVVWLVL
                                                                                       DYFSDTVYIADLIIRLRTGFLEQGLLVKDPKKLRDNYIHTLQFKLDVASIIPTDLIYFAV
                                                                                                                 .81 DYFSDTVZIADLIRLRIGFLEQGLLVKDPKKLRDNYIHTLQFKLDVASIIPTDLIYFAV
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                                                                                                                                                                                                                                                                                                                                                                                                  Rat; G protein-coupled receptor; cyclic nucleotide-gated channel; GPCR; cyclic nucleotide-gated channel; CNG channel.
                     BKLEQLETNMDTLYTRFARLLAEYTGAQQKLKQRITVLETKMKQNHEDDYLSDGINTPEP
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NIRSLGYSDLFCLSKDDLMEAVTEAPDAKKVLEERGREILMKMGLLDENEVAASMEVDVQ
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                Disclosure; Fig 4; 177pp; English.
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                                                                                                      The sequences given in AAG79526-29 represent rabbit, cow, mouse and rat versions of the human cation channel polypeptide designated HBWYCNG. HBMYCNG is a human cyclic nucleotide gated cation channel with six transmembrane domains. HBWYCNG genes are useful for treating ion channel-related disorders, e.g. stroke, anxiety and depression, Alzheimer's or parkinson's disease, arrhythmia, diabetes, chronic pain, hypercalcaemia, hypocalcaemia, hypocalcaemia, agastrointestinal disorders, ion disorders or renal or liver disease
 New human HBMYCNG genes, useful for treating ion channel-related disorders e.g. stroke, anxiety and depression, Alzheimer's or Parkinson's disease, diabetes or arrhythmia.
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New human HBMYCNG genes, useful for treating ion channel-related disorders e.g. stroke, anxiety and depression, Alzheimer's or Parkinson's
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                                                                                                                                                          ion channel-related disorder; stroke; depression; liver disease; Alzheiner's disease, Parkinson's disease; arrhythmia; diabetes; chronic pain; hypercalcaemia; hypocalcaemia; hypercalcaemia; hypercalciuria; anxiety; hypocalciuria; gastrointestinal disorder; renal disease.
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                                                                                                                              cyclic nucleotide gated; HBMYCNG;
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                                                                                                                              cation channel;
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CNG ion channel; alpha3 subunit; phosphodiesterase; drug screening; cyclic nucleotide gated ion channel; champ sensitivity; adenyl cyclase; cyclic adenosine monophosphate; cyclic guanosine monophosphate; cyclic guanosine monophosphate; bovine; G protein-coupled receptor; calcium concentration.
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                                                                                                                            MTEKANGVKSSPANNHNHHAPPAIKASGKDDHRASSRPQSAAA-DDTSSELQQLAEMDAP
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                                                3204.5; DB 5
No. 1.2e-306;
                                               92.2%; Score 3204.5;
92.3%; Pred. No. 1.2e
ive 27; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequences given in AAG79526-29 represent rabbit, cow, mouse and rat versions of the human cation channel polypeptide designated HBMYCNG. HBMYCNG is a human cyclic nucleotide gated cation channel with six transmembrane domains. HBMYCNG genes are useful for treating ion channel-related disorders, e.g. stroke, anxiety and depression, Alzhelmer's or barkinson's disease, arrivthmia, diabetes, chronic pain, hypercalcaemia, hypocalcaemia, hypocalcaemia, hypocalcaemia, adapta disorders or renal or liver disease
                                                                                                                           547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        c treating ion channel-related depression, Alzheimer's or Parkinson's
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                                                                                                                                                                                                                                                                              KLEQLETNMDTLYTRFARLLAEYTGAQQKLKQRITVLETKMKQNHEDDYLSDGINTPEPT 661
                                                                                                                                                                                                                                                                                                  668 KLKQLETNMETLYTRFGRLLABYTGAQQKLKQRITVLEVKMKQNTEDDYLSDGMNSPEPA 727
                                                                                                              YICRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSKMGNRRTAN
                                                                                                                                                                                                                  IRSLGYSDLFCLSKDDLMEAVTEAPDAKKVLEERGREILMKMGLLDENEVAASMEVDVQE
                                                                                                                                                                                                                                         608 IRSLGYSDLFCLSKDDLMEAVTEYPDAKKVLEERGREILMKEGLLDENEVAASMEVDVQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cation channel; cyclic nucleotide gated; HBMYCNG;
ion channel-related disorder; stroke; depression; liver disease;
Alzheimer's disease; Parkinson's disease; arrhythmia; diabetes;
chronic pain; hypercalcaemia; hypocalcaemia; hypercalciuria; anxiety;
hypocalciuria; gastrointestinal disorder; renal disease.
IGFGVDTWVYPNITDPEYGYLAREYIYCLYWSTLTLTTIGETPPPVKDEEYLFVIFDFLI
                                                             GVLIFATIVGNVGSMISNMNATRAEFQAKIDAVKHYMQFRKVSKEMEAKVIKWFDYLWTN
                                                                                          KKTVDEREVLKNLPAKLRAEIAINVHLSTLKKVRI FODWEAGLLVELVLKLRPQVFSPGD
                                                                                                                                                      YICRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSKMGNRRTAN
                                GVLIFATIVGNVGSMISNMNATRAEFQAKIDAVKHYMQFRKVSKDMEAKVIKWFDYLWTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Westphal R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human HBMYCNG genes, useful for disorders e.g. stroke, anxiety and disease, diabetes or arrhythmia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Fig 4; 177pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ramanathan
                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-DEC-2001; 2001WO-US050413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-DEC-2000; 2000US-0257865P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mintier G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-691655/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                            664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COW HEMYCNG
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 368
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359 421 419 481 479 541 539 629

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New genetically modified cyclic nucleotide gated ion channel, useful e.g. for drug screening, has increased sensitivity, or selectivity, for cyclic adenosine monophosphate.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNG ion channel; alpha3 subunit; phosphodiesterase; drug screening; cyclic nucleotide gated ion channel; CAMP sensitivity; adenyl cyclase; cyclic adenosine monophosphate; cyclic quanosine monophosphate; bovine; 6 protein-coupled receptor; calcium concentration; mutain; mutain.
                                                                                                     360 GVLIFATIVGNVGSMISNMMATRAEFQAKIDAVKHYMQFRKVSKEMEAKVIRWFDYLWTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 600 KLEQLETNMDTLYTRFARLLAEYTGAQQKLKQRITVLETKOKQNNEDDSLSDGMNSPEPP
                                                                         GVLIFATIVGNVGSMISNMNATRAEFQAKIDAVKHYMQFRKVSKDMEAKVIKWFDYLWTN
                                                                                                                                                              KKTVDEREVLKNI PAKLRAEIAINVHI STIKKVRI FQDWEAGLLVELVIKIRPQVFSPGD
                                                                                                                                                                                                         420 KKSVDEREVLKNIPAKIRAEIAINVHISTIKKVRIFQDCEAGLLVELVLKIRPQVFSPGD
                                                                                                                                                                                                                                                      YICRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSKMGNRRTAN
                                                                                                                                                                                                                                                                                              480 YICRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSKMGNRRTAN
                                                                                                                                                                                                                                                                                                                                             542 IRSLGYSDLFCLSKDDLMEAVTEAPDAKKVLEERGREILMKMGLLDENEVAASMEVDVQE
                                                                                                                                                                                                                                                                                                                                                                                 540 IRSLGYSDLFCLSKDDLMEAVTEYPDAKRVLBERGREILMKEGLLDENEVAASMEVDVQE
                                                                                                                                                                                                                                                                                                                                                                                                                                       KLEQLETNMDTLYTRFARLLAEYTGAQQKLKQRITVLETKMKQNHEDDYLSDGINTPEPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= T537V
/note= "Wild type Thr is replaced by Val"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovine CNG ion channel alpha3 subunit mutant T537V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Koerschen H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1-4; Page 88-91; 93pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KERJ ) FORSCHUNGSZENTRUM JUELICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG74914 standard; protein; 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gauss R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seifert R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2003-256538/25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003014149-A2
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                                                                         362
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                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This interaction describes a mover genericarry micritical ucyclic decoration corresponding to This37 of the bovine alpha3 subunit is changed so as to corresponding to This37 of the bovine alpha3 subunit is changed so as to corresponding to This37 of the bovine alpha3 subunit is changed so as to corresponding to This37 of the bovine alpha3 subunit is changed so as to selectivity for cAMP over cyclic guanosine monophosphate (cAMP) and/or alpha3 subunit in which the position corresponding to This37 is substituted by any residue except Ser. The products of the invention are used (i) to measure intracellular cAMP concentrations and (ii) to coupled receptors, also of other activators and inhibitors on other process that regulate the intracellular cAMP concentration. Cell lines that express the novel channel are used (i) to measure the intracellular cAMP concentration of pharmacological substances that modulate intracellular cAMP concentration and (ii) to characterise G protein-coupled receptors, and/or pharmacological substances that modulate intracellular cAMP concentration and (ii) to characterise G protein-coupled receptors, adenyl cyclase, phosphodiesterases or other proteins that regulate cAMP, concentration but has the same sensitivity as known double mutants and compared and provides a rapid and simple cellular measuring system that is effective and universally applicable for drug screening and characterisation. This sequence represents the wild type bovine CNG ion channel alpha3 subunit the the interpretation in the disclosure of the characterised in the disclosure of
                                                                                                                                                                                                                                                                                                                                      genetically modified cyclic nucleotide gated ion channel, useful e.g. drug screening, has increased sensitivity, or selectivity, for cyclic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention describes a novel genetically modified cyclic nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 YVSDVVYIADLFIRLRIGFLEQGLLVKDTKKLRDNYIHTMQFKLDVASIIPTDLIYFAVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGKGTKKKFELFVLDPAGDWYYRWLFVIAMPVLYNWCLLVARACFSDLQRNYFVVWLVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YFSDTVYIADLIIRLRIGFLEQGLLVKDPKKLRDNYIHTLQFKLDVASIIPTDLIYFAVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IHSPEVRFNRLLHFARMFEFFDRTETRTSYPNIFRISNLVLYILVIIHWNACIYYVISKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IHNPEVRFNRLLHFARMFEFFDRTETRISYPNIFRISNLILYILIIHWNACIYYAISKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 MTEKSNGVKSSPANNHNHHPPPSIKANGKDDHRAGSRPQSVAADDDTSPELORLAEMDTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6;
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                                                                                                                                                                                                                              H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.2%; Score 3204.5;
92.3%; Pred. No. 1.2e
ive 27; Mismatches
                                                                                                                                                                                                                              Koerschen
                                                                                                                                                                            (KERJ ) FORSCHUNGSZENTRUM JUELICH GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                1; Page 73-76; 93pp; German.
                                                                                                                                                                                                                            Gauss R,
                                                                                       06-AUG-2002; 2002WO-EP008756
                                                                                                                                  38-AUG-2001; 2001DE-01038876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 92.3
es 610; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   adenosine monophosphate.
                                                                                                                                                                                                                         Seifert R,
                                                                                                                                                                                                                                                                    WFI; 2003-256538/25.
N-PSDB; ABX94804.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 663 AA;
WO2003014149-A2
                                            20-FEB-2003
                                                                                                                                                                                                                         UB,
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                                                                                                                                                                                                                         Kaupp
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Matches
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662 A 662

gated (CNG) ion channel which comprises subunits in which the position
corresponding to Thr537 of the bovine alpha3 subunit is changed so as to
increase sensitivity to cyclic adenosine monophosphate (cAMP) and/or
selectivity for cAMP over cyclic guanosine monophosphate (cAMP) and/or
c selectivity for cAMP over cyclic guanosine monophosphate, relative to the
wild type. The invention also describes a modified bovine CNG ion channel
cc alpha3 subunit in which the position corresponding to Thr537 is
substituted by any residue except Ser. The products of the invention are
cused (i) to measure intracellular cAMP concentrations and (ii) to
coupled receptors, also of other activators and inhibitors on other
c proteins that regulate the intracellular cAMP concentration. Cell lines
that express the novel channel are used (i) to measure the intracellular
calcium concentration, especially for characterisation of pharmaceutical
and/or pharmacological substances that modulate intracellular cAMP
concentration and (ii) to characterise G protein-coupled receptors,
adenyl cyclase, phosphodiesterases or other proteins that regulate CAMP,
concentration but has the same sensitivity as known double mutants and
comparation but has the same sensitivity as known double mutants and
coposition but has the same sensitivity as known double mutants and
coportion provines a rapid and simple cellular measuring system that is effective
and universally applicable for drug screening and characterisation. This
cyclase, T537V, described in the disclosure of the invention

Sequence 663 AA;

. . . BGKGTKKKFELFVLDPAGDWYYRNLFVIAMPVLYNWCLLVARACFSDLQRNYFVVWLVLD 181 241 GVLIFATIVGNVGSMISNMNATRAEFQAKIDAVKHYMQFRKVSKEMBAKVIRWFDYLWTN 419 481 541 539 601 121 301 IGEGVDTWVYPNITDPEYGYLAREYIYCLYWSTLTTIGETPPPVKDEEYLFVIFDFLI 361 GVLIFATIVGNVGSMISNMNATRAEFQAKIDAVKHYMQFRKVSKDMEAKVIKWFDYLWTN 421 KLEQLETNMDTLYTRFARLLABYTGAQQKLKQRITVLETKMKQNHEDDYLSDGINTPEPT 661 61 1 MTEKANGVKSSPANNENHHAPPAIKASGKDDHRASSRPQSAAA-DDTSSELQQLAEMDAP 60 QQRRGGFRRIARLVGVLREWAXRNFREEEPRPDSFLERPRGFELHTVTTQQGDKDG IHSPEVRFNRLLHFARMFEFFDRTETRISYPNIFRISNLVLYILVIIHWNACIYYVISKS 240 IHNPEVRENRLIHFARMEBFFDRTETRTSYPNIFRISNLILYILIIHWACIYYAISKS MTEKSNGVKSSPANNHNHHPPPSIKANGKDDHRAGSRPQSVAADDDTSPELQRLAEMDTP RRGRGGFQRIVRLVGVIRDWANKNFREEEPRPDSFLERFRGPELQTVTTHQGDDKGGKDG KKTVDEREVLKNLPAKLRAEIAINVHLSTLKKVRIFQDWEAGLLVELVLKLRPQVFSPGD IRSLGYSDLFCLSKDDLMEAVTEAPDAKKVLEERGREILMKMGLLDENEVAASMEVDVQE YPSDTVYIADLIIRLRTGFLEQGLLVKDPKKLRDNYIHTLQFKLDVASIIPTDLIYFAVG YICRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSKMGNRRTAN Gaps 1; DB 6; Length 663; 24; Indels 92.1%; Score 3199.5; DB 6 92.1%; Pred. No. 3.7e-306; tive 27; Mismatches 24; Query Match
Best Local Similarity 92.19 300 362 360 480 N 122 120 182 242 302 422 482 542 540 602 g g à ď δ 임 à Ωp D à g Db δ 엄 à ò 원 à ð ð

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cave ion channel; alpha3 subunit; phosphodiesterase; drug screening; cyclic nuclectide gated ion channel; cAMP sensitivity; adenyl cyclase; cyclic adenosine monophosphate; cyclic guanosine monophosphate; bovine; G protein-coupled receptor; calcium concentration; mutant; mutein.
                                                                                                                                                                     "Wild type Thr is replaced by Met"
                                                                                        CNG ion channel; alpha3 subunit; phosphodiesterase;
                                                                           Bovine CNG ion channel alpha3 subunit mutant T537M.
                                                                                                                                             Location/Qualifiers
Misc-difference 537
                                   AA.
                                  ABG74913 standard; protein; 663
                                                                                                                                                              /label= T537M
                                                             (first entry)
                                                                                                                                                                     /note=
660 À 660
                                                             10-JUL-2003
                                                                                                                           Bos taurus
                                                                                                                                   Synthetic.
                                               ABG74913;
                    RESULT 13
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20-FEB-2003

WO2003014149-A2

08-AUG-2001; 2001DE-01038876. 06-AUG-2002; 2002WO-EP008756.

(KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.

Koerschen H; Gauss R, Kaupp UB,

2003-256538/25. N-PSDB; ABX94805. New genetically modified cyclic nucleotide gated ion channel, useful e.g. for drug screening, has increased sensitivity, or selectivity, for cyclic adenosine monophosphate.

Example 1-4; Page 81-84; 93pp; German.

direction describes a novel generically monitor.

Gated (CNG) ion channel which comprises bubmit is changed so as to increase sensitivity to cyclic adenosine monophosphate (CAMP) and/or selectivity for CAMP over cyclic adenosine monophosphate, relative to the wild type. The invention also describes a modified bovine CNG ion channel caphal aubunit in which the position corresponding to Thristy is substituted by any residue except Ser. The products of the invention are used (i) to measure intracellular CAMP concentrations and (ii) to coupled receptors, also of other activators and inhibitors on other coupled receptors, also of other activators and inhibitors on other calcium concentration. Cell lines that express the novel channel are used (i) to measure the intracellular CAMP concentration of pharmaceutical and/or pharmacological substances that modulate intracellular CAMP concentration and (ii) to characterise G protein-coupled receptors, and (ii) to characterise G protein-coupled receptors, phosphodiesterases or other proteins that regulate cAMP, concentration and (ii) to characterise G protein-coupled at only one particularly for drug screening. The channel is modified at only one provides a rapid and simple eallular measuring system that is effective and concentration and concentrates or other proteins that regulate cAMP.

Concentration but has the same sensitivity as known double mutants and concentration c This invention describes a novel genetically modified cyclic nucleotide and universally applicable for drug screening and characterisation. The sequence represents the mutant bovine CNG ion channel alpha3 subunit, T537M, described in the disclosure of the invention

Wed May 12

Sequence 663 AA;

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                                                                                                                     Human; transporter and ion channel-7; TRICH-7; vaccine; cystic fibrosis; gene therapy; amyotrophic lateral sclerosis; ammesia; muscular dystrophy; hypertension; angina; neurological disorder; asthma; bipodar disorder; dementia; depression; Alzheimer's disease; epilepsy; mood; arrhythmia; pick's disease; ischaemic cerebrovascular disease; AIDS; anxiety; stroke; Huntington; sdisease; parkinson's disease; cerebral neoplasm; allergy; demyelinating disease; mental disorder; Schizophrenia; polymyositis; muscle disorder; cardiomyopathy; cataract; myocarditis; grave's disease;
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                                                                                                                                                                                                             YFSDTVYIADLIIRLRIGFLEQGLLVKDPKKLRDNYIHTLQFKLDVASIIPTDLIYFAVG 241
                                                                                                                                                                                                                                                                  IHSPEVRFNRLLHFARMFEFFDRTETRTSYPNIFRISNLVLYILVIIHWNACIYYVISKS 301
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                                                                    IGFGVDTWVYPNITDPEYGYLAREYIYCLYWSTLTLTTIGETPPPVKDEEYLFVIFDFLI
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                                                  MTEKSNGVKSSPANNHNHHPPPPSIKANGKDDHRAGSRPQSVAADDDTSPELQRLAENDTP
                           1; Gaps
  Length 663;
                           24; Indels
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92.0%; Score 3198.5; DB 6; 92.1%; Pred. No. 4.7e-306;
                         27; Mismatches
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            Similarity
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Novel human transporter and ion channel proteins useful for treating and preventing transport, neurological, muscle and immunological disorders.

N-PSDB; AAD09558

Claim 1; Page 119-120; 160pp; English.

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J, Lu DAM, Yang J, Reddy R;
Yue H, Nguyen DB, Yao MG, Gandhi AR;
dermatomyositis; diabetes mellitus; immunological disorder; psoriasis; rheumatodi arthritis; Sjogren's syndrome; systemic lupus erythematosus; sickle cell anaemia; Wilson's disease; infertility; Cushing's disease; scleroderma; pulmonary artery stenosis; noctropic; Addison's disease;
                                                                                                                                                                                                                                             /note= "Cyclic nucleotide binding domain"
                                                                                malabsorption syndrome; hypercholesterolaemia; cancer.
                                                                                                                                                                                    160. .476
/label= Transmembrane domain
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/label= Transmembrane_domain
516. 525
/label= Transmembrane_domain
                                                                                                                                                             Location/Qualifiers
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Azimzai Y,
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2000US-0177332P.
2000US-0178572P.
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21-JAN-2000;
28-JAN-2000;
                                                                                                                         Homo sapiens
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10-FEB-2000;
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The present sequence is transporter and ion channel-7 (TRICH-7) protein.

TRICH is used as vaccine. TRICH is useful for treating a disease or condition associated with decreased expression of functional TRICH, such as transport disorder including amyotrophic lateral sclerosis, cystic fibrosis, Becker's muscular dystrophy, Charcot-Marie Tooth disease, Duchenne muscular dystrophy, angina and hypertension, neurological disorders including Alzheimer's disease, amnesia, bipolar disorder, dementia, depression, epilepsy, ischaemic cerebrovascular disorder, etroke, cerebral neoplasmas, Pick's disease, mental disorders including stroke, cerebral neoplasmas, Pick's disease, mental disorders including extinomyopathy, myocarditis, polymyositis, of arthyrhmids and asthma and immunological disorders including arthyrhmids and asthma and immunological disorders including arthyrhmids and asthma and immunological disorders including arthyrhmids and asthma and including AlDS, allergies, anemia, diabetes mellitus, rheumatosia and other diseases including sickle cell anaemia, Wilson's disease, cataracte, infertility, pulmonary arters stenosis, Grave's disease, cataractes, infertility, pulmonary arters stenosis, Grave's disease, cataractes, infertility, pulmonary arters stenosis, Grave's disease, cataractes, infertility, pulmonary arters stenosis, Grave's disease, Cushing's disease, Addison's disease, postiasis and viral, bacterial, fungal, helminthic and protozoal

"Infections TRICH DNA is useful in gene therapy and in diagnostic

Sequence 664 AA;

Query Match
92.0%; Score 3197.5; DB 4; Length 664;
Best Local Similarity 92.3%; Pred. No. 5.9e-306;
Matches 612; Conservative 21; Mismatches 29; Indels 1; Gaps

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                                                                                                                                                                                                The present sequence represents a human ion channel protein (designated NHP). Expression of the NHP transcript on be detected in human testis cells. The gene is encoded on the X chromosome. The protein shares sequence similarity with mammalian cyclic nucleotide-gated ion channel proteins. The nucleic acid and its encoded protein are useful for diagnosis, drug screening clinical trial monitoring, treatment of diseases and disorders, or cosmetic and nutritional application
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                                                                                              New human ion channel protein and polynucleotide, used for diagnosis, drug screening, clinical trial monitoring, treatment of diseases and disorders, or cosmetic and nutritional applications.
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Issued Patents AA: *

Database

Sequence 19, Appl Sequence 46, Appl Sequence 27, Appl Sequence 28, Appl Sequence 22, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 12, Appl Sequence 2, Appli Sequence 3, Appli 21, Appl 4, Appli 23, Appl 22, Appl 36, Appl 9, Appli 11, Appli 13, Description Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence US-09-275-252A-19 US-09-275-252A-18 US-09-358-383C-24 US-09-358-383C-27 US-09-358-383C-27 US-08-997-685A-58 US-08-997-685A-7 US-08-997-685A-10 US-08-997-685A-10 US-08-997-685A-12 US-08-997-685A-12 US-08-997-685A-12 US-09-614-480-2 US-09-614-480-9 US-09-694-777A-21 SUMMARIES 1126 3119 9119 91126 9126 9126 9128 9128 911102 11108 11108 11108 Length 11.7 7 Query Match 448 446 446 440 424.5 424.5 415.5 415.5 413.407.5 407.5 401.3 Score 1323 634 534 573.5 532.5 526.5 523.5 513 486.5 474 423 Result No.

Sequence 13, Appl	Sequence 2, Appli	Sequence 4, Appli		Sequence 12, Appl	Sequence 4, Appli	Sequence 4, Appli	Sequence 6, Appli	Sequence 2, Appli		25,	•	_	Sequence 11, Appl		Æ	Sequence 39, Appl	Sequence 5, Appli
US-09-351-215-13	US-09-226-012-2	US-09-226-012-4	US-09-358-383C-10	US-09-275-252A-12	US-08-956-242-4	US-09-351-215-4	US-09-600-776-6	US-09-600-776-2	US-09-343-494-1	US-09-358-383C-25	US-09-358-383C-2	US-09-336-643A-20	US-09-275-252A-11	US-09-275-252A-38	US-09-275-252A-7	US-09-275-252A-39	US-09-358-383C-5
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394	394	394	394	394	390.5	390.5	385.5	381.5	381.5	381	380	378.5	319.5	300	286.5	265	254
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ALIGNMENTS

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reract	38;
ULT 1 90-275-252A-19 equence 19, Application US/09275252A atent No. 6641997 atent No. 6641997 BENERAL INFORMATION. APPLICANT: MacKinnon, Roderick APPLICANT: The Rockefeller University TITLE OF INVENTION: Assays for Screening Compounds Which Interact With TITLE OF INVENTION: Cation Channel Proteins, and Uses Thereof TITLE OF INVENTION: Cation Channel Proteins, and Uses Thereof CURRENT APPLICATION NUMBER: US/09/275,252A CURRENT FILING DATE: 1999-03-24 PRIOR FILING DATE: 1998-04-02 PRIOR PRILING DATE: 1999-04-02 PRIOR PRILING DATE: 1999-04-02 PRIOR PRILING DATE: 1999-03-2 ROCHANDER: Patentln Ver. 2.1 EQ ID NO 19 TYPE: PRT ORGANISM: Homo sapiens 09-275-252A-19	Length 690; Indels 3
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15252A iversit Soreen annel B Collin S S S S S 9/045,5 9/054,3 CT/US99	<pre>k; Score 2030; DB 4; k; Pred. No. 9.9e-193; 84; Mismatches 131;</pre>
SULT 1 -09-275-252A-19 Sequence 19, Application US/09275252A Parent No. 6641997 CREMENL INFORMATION: APPLICANT: MacKinnon, Roderick APPLICANT: The Rockefeller University APPLICANT: The Rockefeller University TITLE OF INVENTION: Cation Channel Proteins, Mutant Proteins of INVENTION: Cation Channel Proteins, and Uses Thereof FILE REPERENCE: 018512-002901US CURRENT PELICATION NUMBER: US/09/275,252A CURRENT PELICATION NUMBER: US/09/275,252A CURRENT PELICATION NUMBER: US/09/275,252P PRIOR APPLICATION NUMBER: US/09/045,529 PRIOR APPLICATION NUMBER: US/09/045,529 PRIOR APPLICATION NUMBER: US/09/045,529 PRIOR FILING DATE: 1998-03-22 RRIOR APPLICATION NUMBER: WO PCT/US99/06307 PRIOR FILING DATE: 1999-03-22 RRIOR APPLICATION NUMBER: WO PCT/US99/06307 PRIOR FILING DATE: 1999-03-22 SEQ ID NO 19 LENGHH: 690 TYPE: PRI ORGANISM: Homo sapiens	
ULT 1 09-275-2524-19 equence 19, Application US/095 atent No. 664197 ENERAL INFORMATION. APPLICANT: The McKinnon, Roderich APPLICANT: The McKinnon, Roderich TITLE OF INVENTION: Assays for TITLE OF INVENTION: Cation C! FILE REFERENCE: 018512-002901 CURRENT APPLICATION NUMBER: US CHENCY RILING DATE: 1999-03-20 PRIOR PLILING DATE: 1999-03-20 PRIOR FILING DATE: 1999-03-20 PRIOR FILING DATE: 1999-03-20 PRIOR FILING DATE: 1999-03-20 NUMBER OF SEQ ID NOS: 42 LENGRER OF SEQ ID NOS: 42 LENGRER OF SEQ ID NOS: 42 LENGRER OF SEQ ID NOS: 42 LENGRER: PATENTIN UNIVER: WO LENGRANISM: Homo sapiens 09-275-252A-19	Query Match Best Local Similarity 61.7 Matches 407; Conservative
SULT 1 -09-275-2524-19 Sequence 19, Applica Sequence 19, Applica Sequence 19, Applica GENERAL INFORMATION: APPLICANT: MacKinno APPLICANT: THE ROC TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: FILE REFERENCE: 018 CURRENT APPLICATION CURRENT APPLICATION CURRENT FILING DATE: PRIOR APPLICATION N PRIOR PILING DATE: PRIOR PILING DATE: NUMBER OF SEQ ID NO SOFTWARE: PATCHTLING SOFTWARE: PATCHTLING SEQ ID NO 19 LEAGTH: 690 LYPE: PRI CREATING DATE: NUMBER OF SEQ ID NO SEQ ID NO 19 LEAGTH: 690 LYPE: PRI CREATING DATE: NUMBER OF SEQ ID NO SEQ ID NO 19 LEAGTH: 690 LYPE: PRI CREATING DATE: NUMBER OF SEQ ID NO SEQ ID NO 19 LEAGTH: 690 LEAGTH: 690 LYPE: PRI CREATING DATE: PRIOR PILING DATE: NUMBER OF SEQ ID NO SEQ ID NO 19 LEAGTH: 690 LEAGTH:	Query Match Best Local Similarity Matches 407; Conserv
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23 PSIKANGKDDHRAGSRPQSVAADDDTSPELQRLAEMDTPRRGRGGF-

81 QYLPGAIAIFNVNNSSNKDQEPEEKKKKKKEKKSKSDDKNENKNDPEKK----KKKKDKE 136

137 KKKKEEKSKDKKEHHKKEVVVIDPSGNIYYNWLFCIILPVMYNWTWVIARACFDELQSDY

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118 GKDGEGKGTKK----KFELFVLDPAGDWYYRWLFVLAMPVLYNWCLLVARACFSDLQRNY

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257 DLLYFKLGWNYPEIRLNRLLRFSRMFEFFQRTETRTNYPNIFRISNLVMYIVIIIHWNAC 316

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234 DLIYFAVGIHSPEVRFNRLLHFARMFEFFDRTETRTSYPNIFRISNLVLYILVIIHWNAC

197 LEYWLILDYVSDIVYLIDMFVRTRTGYLEQGLLVKEELKLINKYKSNLQFKLDVLSLIPT

174 FVVWLVLDYFSDTVYIADLIIRLRTGFLEQGLLVKDPKKLRDNYIHTLQFKLDVASIIPT

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Sequence 46 Application US/08997685A
Patent No. 6551821
GENERAL INFORMATION:
A APPLICANT: The Trustees of Columbia University
APPLICANT: Tandel, Eric
TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
TITLE OF INVENTION: UNMBER: US/08/997,685A
CURRENT APPLICATION UNMBER: US/08/997,685A
NUMBER OF SEQ ID NOS: 60
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TILLE NEFERENCE: MNI-0522 POTASSIUM CHANNEL MOLECULES AND USES THEREFOR FILE REFERENCE: MNI-0522 POTASSIUM CHANNEL MOLECULES AND USES THEREFOR CURRENT APPLICATION NUMBER: US/09/358,383C
CURRENT FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: USN 09/119,855
PRIOR FILING DATE: 1998-07-21
NUMBER OF SEQ ID NOS: 36
SSC TRARE: PATENTIN Ver. 2.0
SSC TRARE: PATENTIN Ver. 2.0
LENGTH: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   464 LLVELVLKTRPQVFSPGDYICRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LLVELVLKLRPQVFSPGDYICRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGE
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                           241 MGNRRTANIRSLGYSDLFCLS 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (48). (49)
OTHER INFORMATION: gap in alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: NON CONS
LOCATION: (125)..(126)
COTHER INFORMATION: gap in alignment
US-08-997-685A-46
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. Sequence 27, Application US/09358383C
. Patent No. 6518398
. GENERAL INFORMATION:
534 MGNRRTANIRSLGYSDLFCLS
                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.1
SEQ ID NO 46
LENGTH: 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: NON CONS
LOCATION: (121)..(122)
OTHER INFORMATION: gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: NON_CONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: rat;
                                                                                                                 RESULT 3
US-08-997-685A-46
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Sequence 18, Application US/0927552A

Sequence 18, Application US/0927552A

Sequence 18, Application US/0927552A

GENERAL INFORMATION:

APPLICANT: MacKinnon, Roderick

APPLICANT: MacKinnon, Roderick

APPLICANT: The Rockefeller University

TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation

TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation

TITLE OF INVENTION: Cation Channel Proteins, and Uses Thereof

FILE REFERRENCE: 018512-002901US

CURRENT FILING DATE: 1999-03-22

PRIOR PELING DATE: 1999-03-22

PRIOR PELING DATE: 1999-03-22

PRIOR FILING DATE: 1999-03-22

NUMBER OF SEC ID NOS: 42.
                                                                                                                                                                                                                                     414 WFDYLWTNKKTVDEREVLKNLPAKLRAEIAINVHLSTLKKVRIFQDWEAGLLVELVLKLR 473
                                          557 AGNRRTANIKSIGYSDLFCLSKDDLMEALTEYPDAKTMLEEKGKQILMKDGLLDINIANA 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              593 ASMEVDVQEKLEQLETNMDTLYTRFARLLAEYTGAQQKLKQRITVLETKMKQNHEDDYLS 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            617 GSDPKDLEEKVTRMEGSVDLLQTRFARILAEYESMQQKLKQRLTKVEKFLKPLIDTEFSS 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 FVIFDFLIGVLIFATIVGNVGSMISNMNATRABFQAKIDAVKHYMQFRKVSKGMEAKVIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          474 PQVFSPGDYICRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSK 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WFDYLWINKKIVDEREVLKNLPAKLRAEIAINVHLSTLKKVRIFQDWEAGLLVELVLKLR 473
                                                                                                                                                                                                                                                                                                      PQVFSPGDYICRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSK 533
                                                                                                                                                                                                                                                                                                                                                                                                   MGNRRTANIRSLGYSDLFCLSKDDLMEAVTEAPDAKKVLEERGREILMKMGLLDENEV-A 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294 IYYVISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWSTLTTLTTIGETPPPVKDEEYL 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FVIFDFLIGVLIFATIVGNVGSMISNMNATRAEFQAKIDAVKHYMQFRKVSKDMEAKVIK 413
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38.1%; Score 1323; DB 4;
Best Local Similarity 97.7%; Pred. No. 4.3e-123;
Matches 255; Conservative 2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JULT 2
-09-275-252A-18
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TYPE: PRT
ORGANISM: bovine;
FEATURE:
NAME/KEY: NON_CONS
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APPLICANT: The Trustees of Columbia University
APPLICANT: The Trustees of Columbia University
APPLICANT: The Trustees of Columbia University
APPLICANT: Kandel, Eric
TILE OF INVARION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
FILE REFERENCE: 0575/54806
FILE REFERENCE: 0575/54806
CURRENT APPLICATION NUMBER: US/08/997,685A
CURRENT APPLICATION NUMBER: US/08/997,685A
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin version 3.1
SEQ ID NO 58
LENGTH: 126
                                                                                                                     289 HWNACIYYVISKSIGFGVDTWVYPNITDPEY-----GYLAREYIYCLYWSTLTLTTIG-E 342
                                                                                                                                                                                                                              61 MPSPTTSFEYVEVFEVFOFLYGVLIFATIIGNYGSMINNAARTEFQNKMDGVKQYMKYRK 120
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                                                                                                                                                                                                        343 TPPPVKDEEYLFVIFDFLIGVLIFATIVGNVGSMISNMNATRAEFQAKIDAVKHYMQFRK 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     522 GEISIINIKGSKMGNRRTANIRSLGYSDLFCLSKDDLMEAVTEAPDAKKVLBERGREILM 581
                                                                                                                                             1 AGLIVEL-LYLRPQVYSPGDYICRKGDIGKEMYIIKEGQLAVVADDGVTQFALLTAGGCF
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16.5%; Score 573.5; DB 4; Length 126;
Best Local Similarity 89.8%; Pred. No. 4.6e-49;
Matches 114; Conservative 7; Mismatches 5; Indels 1
                                       16.8%; Score 584; DB 4; Length 170; 62.9%; Pred. No. 6.9e-50; ive 21; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: NON CONS
LOCATION: (477..(48)
OTHER INFORMATION: gap in alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 58, Application US/08997685A; Patent No. 6551821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (7). (8)
OTHER INFORMATION: gap in alignment
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OTHER INFORMATION: gap in alignment
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LOCATION: (667..(67)
OTHER INFORMATION: gap in alignment
                                     Query Match
Best Local Similarity 62.9
Matches 107; Conservative
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NAME/KEY: NON CONS
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NAME/KEY: NON CONS
LOCATION: (56)..(5
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ORGANISM: catfish;
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US-08-997-685A-58
US-09-358-383C-27
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US-08-997-685A-58
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RESULT 6 US-09-358-383C-22

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Sequence 57. Application US/08997685A
Patent No. 6551021
GENERAL INFORMATION:
APPLICANT: The Trustees of Columbia University
APPLICANT: The Trustees of Columbia University
APPLICANT: APPLICANT: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof;
TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof;
CURRENT FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn version 3.1
SEQ ID NO 57
INNER: PATENT IN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 FEEPSLWTRGITGGPSLKRQYITSLYWSITTLTTVGYGDPAPVTTREKIFVIFDMLFGVL 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       270 SYPNIF--RISNLVLYILVIIHWNAC----IYYVIS-----KSIGFGVDTWVYPNITD 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AF-NYFAIRLIKLVCVTLLIHWNACVFDILLYYLISDYDVBAERYGFGTDTWLYALNND 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         317 PEY------GYLAREYIYCLYWSTLTLTTIG-ETPPPVKDEEYLFVIFDFLIGVL 364
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Sequence 22, Application US/09358383C
BREENL NO. 6518398
GENERAL INFORMATION:
APPLICANT: Curtis, Rory A.J.
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR FILE REFERENCE: MXI-055CP
CURRENT APPLICATION NUMBER: US/09/358,383C
CURRENT FILING DATE: 1999-07-21
FRIOR APPLICATION NUMBER: USN 09/119,855
FRIOR APPLICATION NUMBER: USN 09/119,855
FRIOR PILING DATE: 1998-07-21
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
LENGTH: 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence: domain US-09-358-383C-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
15.3%; Score 532.5; DB 4;
Best Local Similarity 45.1%; Pred. No. 2.5e-44;
Matches 125; Conservative 37; Mismatches 74;
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OTHER INFORMATION: gap in alignment
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; OTHER INFORMATION: gap in alignment US-08-997-685A-57
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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Sequence 10, Application US/08997685A
Patent No. 6551821
APPLICANT: Kandel, Eric
TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
FILE REFERENCE: 0575/54806
CURRENT APPLICATION NUMBER: US/08/997,685A
CURRENT APPLICATION NUMBER: US/08/997,685A
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn version 3.1
LENGTH: 749
TYPE: PRT
      28;
                                                                                                                       108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269 QWEEIFHMTYDLASAVVRIFNLIGMMLLLCHWDGCLQFLVPLLQDFPPDCWVSLNEMVND 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 EEPAGSFEDAEGPRROYGFMOR--OFTSMLOPGVNK-----FSLRMFGSO---- 106
                                                                                                                                                                                                  109 TTHQGDDKGGKDGEGKGTKKKFE-----LFVLDPAGDWYYRWLFVIAMPVLYNWCLLVA 162
                                                                                                                                                                                                                            163 RACFSDLQRNYFVVWLVLDYFSDTVYIADLIIRLRTGFL--EQGLLVKDPKKLRDNYIHT 220
                                                                                                                                                                                                                                                                                                       221 LQFKLDVASIIPTDLIYFAV--GIHSPE------VRFN------RLLHFARMFEFFD 263
                                                                                                                                                                                                                                                                                                                                                                                     210 -WFVVDFISSIPVDYIFLIVEKGMDSEVYKTARALRIVRFTKILSLIRLIRLSRLIRYIH 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  377 ISNMMATRAEFQAKIDAVKHYMQFRKVSKDMEAKVIKWFDYLWTNKKTVDEREVLKNLPA 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         386 IQSLDSSRRQYQEKYKQVEQYMSFHKLPADMRQKIHDYYEHRYQG-KIFDENILSELND 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                437 KLRAEIAINVHLSTL-KKVRIFQDWEAGLLVELVLKLRPQVFSPGDYICRKGDIGKEMYI 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             496 IKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSKMGNRRTANIRSLGYSDLFCLSK 555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 GGKPNSASNSRDDGNSVFPSKAPATGPVAADKRLGTPPRGGAAGKEHGNSVCFKVDGGGG
                                                                                                                       53 ----QRLAEMDTPRRGRGGFQRIVRLVGVIRDWANKNFREBEPRPDSFLERFRGPELQTV
                                                                                                                                                                                                                                                                                                                                                                                                                                       264 RTE----TRISYPNIFRISNLVLYILVIIHWNACIYYVISKSIGFGVDTWVYPN-ITDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     318 EYGYLAREYIYCLYWSTLTLTTTG-ETPPPVKDEEYLFVIFDFLIGVLIFATIVGNVGSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   597 VDVQEKLEQLETNMDTLYTRFARL--LAEYTGAQQKLKQRITVLETKMKQNHEDDYL-SD
      Gaps
      125;
                                           8 GVKSSPANNH-----NHHPPPSIKANG--KDDHRAGSRPQSVAADDDTSPEL-
      Indels
      180; Conservative 137; Mismatches 287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       673 STQTPQPSA 681
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PUBLICATION INFORMATION:
                                                                                                                                                                                                                                         107 ----
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US-08-997-685A-10
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Patent No. 6551821
GENERAL INFORMATION:
APPLICANT: The Trustees of Columbia University
APPLICANT: Kandel, Eric
TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
                                                                                                                                                            521
                                                                                                                                      GEISILNIKGSKMGNRRTANIRSLGYSDLFCLSKDDLMEAVTEAPDAKKVLEERGREILM 581
                                                                                                 59
                                                         462 AGLLVELVLKLRPQVFSPGDYICRKGDIGKEMYIIKEGKLAVVADDGVTQXALLSAGSCF
                                                                                    1 AGLIAVELVIXLOPQVYS-GDYICKKGDIGREMYIIKEGKLAVVADDGITOFVVLSDGSYF
                      Gaps
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                      Indels
  82.5%; Pred. No. 2.2e-44;
ive 14; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/08/997,685A CURRENT FILTHS DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin version 3.1
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DATABASE ENTRY DATE: 1997-12-27
RELEVANT RESIDUES: (1)..(910)
US-08-997-685A-2
Best Local Similarity 82.5
Matches 104; Conservative
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LOCATION: (472)..(602)
OTHER INFORMATION: CNB
PUBLICATION INFORMATION.
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LOCATION: (291)..(313)
OTHER INFORMATION: S5
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OTHER INFORMATION: P
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OTHER INFORMATION: S2
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OTHER INFORMATION: S4
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OTHER INFORMATION: S6
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OTHER INFORMATION: S3
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Best Local Similarity
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NAME/KEY: DOMAIN
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US-08-997-685A-2
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APPLICANT: The Trustees of Columbia University
APPLICANT: The Trustees of Columbia University
APPLICANT: Randel, Eric
TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
FILE REPERENCE: 0575/54806
CURRENT APPLICATION NUMBER: US/08/997,685A
CURRENT FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin version 3.1
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            417 TKG--NKEMKLSDGSYFGEICLIT-----RGRRTASVRADTYCRLYSLSVDNFNEVLEE 468
                                                                                   121 GEGKGTKKKFE-----LFVLDPAGDWYYRWLFVIAMPVLYNWCLL-VARACFSDLQRNY 173
                                                                                                                                                                                                                                                                   241 ALFKAMSHMLCIGYGRQAPESMTD--IWLTMLSMIVGATCYAMFIGHATALIQSLDSSRR 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   270 SYPNIFRISNLVLYILVIIHWNACIYYVISKSIGFGVDTWV-YPNITDPEYGYLAREYIY 328
                                                                                                                                                                                                                                                                                                                                                                                                 CLYWSTLTLTIG---ETPPPVKDEEXLFVIFDFLIGVLIFATIVGNVGSMISNMNATRA 385
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                                                                                                          | | ::: | :: | | :: | | | CSQKAVEREQERVKSAGAWIIHPYSDFRYWDFTMLLFWWGNLIIIPWGIIFFKD---ET
                                                                                                                                                                                     PIDLIYFAV--GIHSPEVR-----TRT
                                                                                                                                                                                                                                                                                                                                            90 BPRPD--SFLERFRGPELQTVTTHQGDDKGG--KDGEGKGTKKKFE-----LFVLDPAG
                                                                                                                                                               174 FVVWLVLDYFSDTVYIADLIIRLRIGFL--BOGLLVKDPKKLRDNYIHTLOFKLDVASII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             386 EFQAKIDAVKHYMQFRKVSKDMEAKVIKWFDYLWTNKKTVDEREVLKNLPAKLRAEIAIN
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                                                   Gaps
                                              55;
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            Length 528;
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Best Local Similarity 26.9%; Pred. No. 4.7e-30;
Matches 144; Conservative 111; Mismatches 216; Indels
                                              Indels
      Ouery Match
14.0%; Score 486.5; DB 4;
Best Local Similarity 26.6%; Pred. No. 2.2e-39;
Matches 133; Conservative 109; Mismatches 203;
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ORGANISM: human;
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AAC39760
DATABASE ENTRY DATE: 1998-05-29
RELEVANT RESIDUES: (1)..(597)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 12, Application US/08997685A; Patent No. 6551821
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TYPE: PRT
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                                                                                                                                                                           133 FVLDPAGDWYXRWLFVIAMPVLYNWCLLVARACFSDLQRNYFVVWLVLDYFSDTVYIADL 192
                                                                                                                                                                                                                                                                               476 KNSILLÖKFQKDLNTGVFNNQENEILKQI---VKHDREMVQAIAPINYPQMTTLNSTSST 532
                                                                                                                                                                                                                                                         IIRLRIGEL -- EQGLLVKDPKKLRDNYIHTLQFKLDVASIIPTDLIYFAV -- GIHSPE-- 246
                                                                                                                                                                                                                                                                                                                                  -----VRFN-----RLLHFARMFEFFDRTE----TRISYPNIFRISNLVLYILVII 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               364 TAMLSKLRFEVFQPGDYIIREGAVGKCMYFIQHGVAGVITKS--SKEMKLTDGSYFGEIC 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                526 ILNIKGSKMGNRRTANIRSLGYSDLFCLSKDDLMEAVTEAPDAKKVLEERGREILMKMG- 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -- DENEVAASMEVDVQEKLEQLETNMDTLYTRFARL--LAEY 624
                                                                                                                                                                                                   12 WIIHPYSDERFYWDLIMLIMMYGNLVIIPYGITFFTEQTT--TPWIIFNVASDTVFLLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                        246 VSMSDLWITMLSMIVGATCYAMFVGHATALIQSLDSSRRQYQEKYKQVEQYMSFHKLPAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VKDEEYLFVIFDFLIGVLIFATIVGNVGSMISNMNATRAEFQAKIDAVKHYMQFRKVSKD
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APPLICANT: Kandel, Eric
TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses
FILE REFERENCE: 0575/54806
CURRENT APPLICATION NUMBER: US/08/997,685A
CURRENT FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
                                                                                                                                          Gaps
                                                                                                                                          68;
                                                                                                    DB 4; Length 749;
                                                                                               14.8%; Score 513; DB 4; Length 746 ilarity 26.3%; Pred. No. 9e-42; Conservative 122; Mismatches 237; Indels
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DATABASE ENTRY DATE: 1998-05-29
RELEVANT RESIDUES: (1)..(749)
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; DATABASE ENTRY DATE: 1998-05-29;
; RELEYANT RESIDUES: (1)..(504)
US-08-997-685A-4
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Patent No. 6551821
GENERAL INFORMATION:
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                                                                                             Query Match
Best Local Similarity
Matches 152; Conserv
                                              ; KELEVANT KESTI
US-08-997-685A-10
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US-08-997-685A-4
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|: ::: | | | | | : : : | | | | : : 256 CLQFLVPMLQDFPHDCWVSINGWVNNSWG---KQYSYALFKAMSHMLCIGYGRQAPVGMS 312
                                                                                                                                                                                                                                                                                                                                                                    313 DVWLJMLSMIVGATCXANFIGHATALIQSLDSSRRQYQEKYKQVEQYMSFHKLPPDTRQR 372
             RTGIVVEDNIEIILDPQRIKMKYLKS-WFVVDFISSIPVEYIFLIVETRIDSEVYKTARA 195
                                                                            TRISYPNIFRISNLVLYILVIIHWNA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                        411 VIKWFDYLWTNKKTVDEREVLKNLPAKLRAEIAINVHLSTL-KKVRIFQDWEAGLLVELV 469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     381 NTIQIDSWLYQLALSIGTP-YRYNTSAGIWEGGPSKDSLYVSSLYFTWTSLTTIGFGNIA 439
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                                                                                                                                                                                                    CIYYVISKSIGFGVDTWVYPN-ITDPEYGYLARBYIYCLYWSTLTLTTIG-ETPPPVKDE
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                                                                                                                 196 VRIVRFTKILSLLRLLRLSRLIRYIHOWEEIFHMTYDLASAVVRIVNLIGMMLLLCHWDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   470 LKLRPQVFSPGDYICRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNI
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llarity 25.2%; Pred. No. 6.5e-35;
Conservative 102; Mismatches 220
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APPLICANT: Jegla, Timothy James
APPLICANT: Jegla, Timothy James
APPLICANT: Jegla, Timothy James
APPLICANT: Jegla, Timothy James
TITLE OF INVENTION: Buman Eag2
FILE OF INVENTION: Buman Eag2
FILE APPLICATION NUMBER: US/09/614,480
CURRENT FILING DATE: 2000-05-29
FRIOR ELLING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 9
                                                                         ---VRFN-----RLLHFARMFEFFDRTE-
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SEQ ID NO 2
LENGTH: 988
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Sequence 6, Application US/08997685A
Patent No. 651821
GENERAL INFORMATION:
APPLICANT: The Trustees of Columbia University
FILE REFERENCE: 0575/54806
CURRENT APPLICATION NUMBER: US/08/997,685A
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Version 3.1
FENCENCE: SEQ ID NOS: 60
SEQ ID NOS: 60
SEQ ID NOS: 60
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DEREYWDFTMLLFMVGNLIIIPVGITFFRD---ETTAPWIVENVYSDTFFLMDLVLNFRT 119
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                                                                                                                                  295 YYVISKSIGFGVDTWVXPN-ITDPEYGYLAREYIYCLYWSTLTLTTIG---ETPPPVKDE 350
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                                                                                                                                                                                                                                                             OFLVPMLQDFPRNCWVSINGMVNHSWSEL---YSFALFKAMSHMLCIGYGRQAPESMTD-
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                                                                                                GFL--EQGLLVKDPKKIRDNYIHTLQFKLDVASIIPTDLIYFAV--GIHSPE-----
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ilarity 25.0%; Pred. No. 1.4e-35;
Conservative 111; Mismatches 212; Indels 100;
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DATABASE ACCESSION NUMBER: AAC40126
DATABASE ENTRY DATE: 1998-05-29
RELEVANT RESIDUES: (1). (506)
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Best Local Similarity
Matches 141; Conserv
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US-08-997-685A-6
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ORGANISM: Homo sapiens
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 ; NUMBER OF SEQ
; SOFTWARE: Fast
; SEQ ID NO 5
; LENGTH: 988
; TYPE: PRT
                                              US-10-162-012-5
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                             466 VELVLKLRPQVFSPGDYICRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEIS 525
                                      ---WKETTLAH-ACANVRALIYCDLHIIKREALLKVLDFYTAFANSFSRNLTLTCNLRKR 673
                                                                                       ---TBAPDAKKVLEERGREILMKWGLLDENEVAASMEVD-----VQEKLEQL----- 606
406 DMEAKVIKWEDYLWINKKTVDBREVLKNLPAKLRAEIAINVHLSTLKKVRIFQDWEAGLL 465
              GLSERVMDYIVSTWSMSKGIDTEKVLSICPKDMRADICVHINRKVFNEHPAFRLASDGCL 559
                                                                                                    674 IIFRKISDVKKEEEERLRQ------KNEVILSIPVDHPVRKLFOKFKQQKELRNQGS 724
                                                                                                                               ----ETINMDTLYTRFARLLAEYTGAQQXLKQRITVLET-----KMKQNHED
                                                         526 ILNIKGSKMGNRRTANIRSLGYSDLFCLSKDDLMEAV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/290,288
FILING DATE: 2001-05-11
APPLICATION NUMBER: US (not assigned)
FILING DATE: 2002-05-13
                                                                                                                                                                        Sequence 5, Application US/10162012
Patent No. 6682597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 GLLVKDPKKLRDNYIHTLOFKLDVASIIPTDLI----YFAVGIHS--PEVRFNRLLHFAR 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----YIYCLYWSTLTLTTIG-ETPP 345
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CURRENT APPLICATION NUMBER: US/10/162,012
CURRENT FILING DATE: 2002-06-06
PRIOR PLICATION NUMBER: US 60/209,845
PRIOR FILING DATE: 2000-06-06
PRIOR PLICATION NUMBER: US 99/875,321
PRIOR PLING DATE: 2001-06-06
PRIOR PLING DATE: 2001-06-06
PRIOR PLING DATE: 2001-06-06
PRIOR PLING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
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PRIOR FILING DATE: 2001-06-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  507 ----ETINMDILYTRFARLLAEYIGAQQKLKQRITVLET------KMKQNHED 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       258 MFEFFDRTETRISYPNIFRISNLVLYILV----IIHWNACIYYVISKSIG-----
                                                                                                                                                                                                                                                                                                             124;
                                                                                                                                                                                                                                            Length 988;
                                                                                                                                                                                                                                            Query Match
12.8%; Score 446; DB 4; Length 98
Best Local Similarity 25.2%; Pred. No. 6.5e-35;
Matches 150; Conservative 102; Mismatches 220; Indels
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SEQ ID NOS: 48
FastSEQ for Windows Version 4.0
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APPLICANT: Siloa-Santiago, Inmaculada
APPLICANT: Gu, Wei
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Sequence 12, Application US/10162012;
Patent No. 6682597
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us-10-087-217a-8.rai

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334 VARKLD------HYLEYGAAVLVLLVCVFGLVAHWLACIWY----SIGDYEVIDEVT 380
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PRIOR APPLICATION NUMBER: US 09/875,423
PRIOR FILING DATE: 2001-06-05
PRIOR PELING DATE: 2001-06-05
PRIOR PILING DATE: 2001-06-05
PRIOR PILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: US 60/209,236
PRIOR PILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: US 09/875,363
PRIOR APPLICATION NUMBER: US 00/227,068
PRIOR APPLICATION NUMBER: US 60/227,068
PRIOR APPLICATION NUMBER: US 60/227,068
PRIOR APPLICATION NUMBER: US 09/228,530
PRIOR APPLICATION NUMBER: US 09/228,530
PRIOR APPLICATION NUMBER: US 09/228,530
PRIOR PILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: US 60/226,770
PRIOR APPLICATION NUMBER: US 60/226,770
PRIOR PILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: US 60/226,770
PRIOR PILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: US 60/226,770
PRIOR PILING DATE: 2001-08-13
PRIOR PILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/29,281
PRIOR APPLICATION NUMBER: US 60/290,288
PRIOR APPLICATION NUMBER: US 60/290,288
PRIOR PILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 60/290,288
PRIOR PILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 60/290,288
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PRIOR APPLICATION NUMBER: US 60/290,288
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PRIOR APPLICATION NUMBER: US 60/290,288
PRIOR PILING DATE: 2001-03-28
PRIOR PILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 60/290,288
PRIOR PILING DATE: 2001-05-13
PRIOR APPLICATION NUMBER: US 60/290,288
PRIOR PILING DATE: 2001-05-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 12.7%; Score 440; DB Best Local Similarity 25.0%; Pred. No. 2.6e Matches 149; Conservative 104; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
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674 IIFRKISDVKKEEEERLRQ-----KNEVTLSIPVDHPVRKLFOKFKOOKELRNOGS 724
| : : : ||:|:| | || : : : 673
                                                                                                                                                                                 725 AQSDPERSQLQVESRPLQNGASITGTSVVTVSQITPIQTSLAYVKTSETLKQNNRD 780
                                                                                                                                                   607 ----ETNMDTLYTRFARLLAEYTGAQQKLKQRITVLETK------MKQNHED 648
                                                               563 ---TEAPDAKKVLEERGREILMKMGLLDENEVAASMEVD--
                                                                                                                                                                                                                                                            Search completed: May 12, 2004, 11:16:21
Job time : 25 secs
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

May 12, 2004, 11:07:49; Search time 17 Seconds Run on:

(without alignments) 2033.799 Million cell updates/sec

US-10-087-217A-8 3475

1 MMTEKSNGVKSSPANNHNHH.......NHEDDYLSDGINTPEPTAAE score: Sequence: Perfect

664

Gapop 10.0 , Gapext 0.5 Scoring table:

BLOSUM62

141681 segs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

141681

seq length: 0 seq length: 2000000000 DB Minimum I Maximum I Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	000195 rattus norv	398	_		gall	mus mus	bog	Q16281 homo sapien		Q90980 gallus galī	-dubb q	h cgmp-	r cgmp-	c cdmb-	E	H	024278 drosophila			homod	L bos t	Q9jkb0 rattus norv	O88704 mus musculu	Q9jka9 rattus norv	O88703 mus musculu	Н	060741 homo sapien	Q9y3q4 homo sapien	rattu	Q9tv66 oryctolagus	_	m	m
SUMMARIES	ΩΙ	CNG2 RAT	CNG2 WOUSE	CNG2 RABIT	CNG2 BOVIN	CNG1 CHICK	CNG3 MOUSE	CNG3 BOVIN	CNG3 HUMAN	н	1	- 1	CNG1 HUMAN		CNG1 CANFA	CNG1_MOUSE	CNGX RAT	CNG DROME	CNG_CAEEL	CNG2 HUMAN	CNG4 HUMAN	CNG4_BOVIN	HCN1_RAT	HCN1_MOUSE	HCN2 RAT	HCN2 MOUSE	HCN1 RABIT	HCN1 HUMAN	HCN4 HUMAN	HCN4 RAT	HCN4 RABIT	HCN2 HUMAN	HCN3 RAT	HCN3_HUMAN
	DB	п	Н	Н	Н	Н	H	H	П	Н	н	Н	н	Н	н	Н	Н	Н	н	Н		Н	П	Н	Н	Н	Н	Н	н	Н	П	Н	Н	Н
	Length	664	664	664	663	735	631	706	694	682	645	690	989	683	691	684	575	665	733	261	606	1394	910	910	834	863	822	890	1203	1198	1175	889	780	774
*	Query Match	99.3	7	3	N	3	61.9	61.6	61.6	61.3	59.5	58.8	58.5	58.3					38.5	38.1	22.4	22.2	15.1	15.0	15.0	15.0	15.0	14.9		4,	4,	14.1		13.8
	Score	3449	3384	3231.5	3204.5	2219.5	2151.5	2140	2139	2131	2067	2044	2034	2026	2017.5	2012.5	1518	1494	1338.5	1323	778	770	524	522.5	522	522	520.5	518	494.5	492	490.5	490	481.5	479
	Result No.	н	73	e	4	ហ	ø	7	ω	σ	10	TT.	12	13	74	15	9 T	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

SMART; SM00100; CNMP; 1.

PROSITE; PS00888; CNMP_BINDING_1; 1.

PROSITE; PS00889; CNMP_BINDING_2; 1.

PROSITE; PS50042; CNMP_BINDING_3; 1.

Ionic channel; Ion transport; CAMP-binding; Transmembrane; Multigene family; Olfaction.

EMBL, X55519; CAA39135.1; -.
PIR, S11517; S11517.
InterPro; IPR000595; COMP. binding.
InterPro; IPR005821; Ion_trans.
InterPro; IPR001622; K+channel_pore.
Pfam; PF00027; coMP. binding; 1.
Pfam; PF00520; ion_trans; 1.

O88705 mus musculu O70507 mus musculu	Q8ncm2 homo sapien Q9epi9 rattus norv	054853 rattus norv	034832 rattus norv Q9er47 mus musculu 095259 homo sapien	Q60603 mus musculu O18965 bos taurus	Q9h252 homo sapien
HCN3_MOUSE	KCHS_HUMAN KCHS_RAT	KCH6 RAT	KCH7 MOUSE KCH1 HUMAN	KCH1 MOUSE	KCH6_HUMAN
пп	η η ,	-		44	ч
779	9 6 6 6 8 8 6 6	950	1195	989 987	994
13.8	12.6	75.0	175.0	12.0	11.9
479	446	418.5	417.5	417	414.5
34	37	0 W 4	4 4 1 2 2 4	4 4 4	45

ALIGNMENTS

RESULT 1

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TISSUENCE FROM N.A.

TISSUE-Olfactory sensory neuron;

TISSUE-Olfactory sensory neurons may be considered to a cyclic nucleotide-

TISSUE Alba-187(1990)

TISSUE Alba-187(1990)

TISSUE SPECIFICATY SIGNAL LANGE AS SECOND messenger. The colfactory channel can be shown to be activated by cyclic nucleotides which leads to a depolarization of olfactory sensory neurons

TISSUE SPECIFICATY: Olfactory neurons.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation — the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch/-sib.ch/.
                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                    01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-DR-2004 (Rel. 43, Last annotation update)
Cyclic-nucleotide-gated olfactory channel (Cyclic-nucleotide-gated cation channel 2) (CNG channel 2) (CNG-2) (OCNC1).
                          664 AA.
                       PRT;
                       STANDARD;
                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                    CNGA2 OR CNCG2
                       RAT
                       CNG2
CNG2_RAT
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                                              MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GEGKGTKKKFELFVLDPAGDWYYRWLFVIAMPVLYNWCLLVARACFSDLORNYFVVWLVL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGEGUDIWUYPNIIDPEYGYLAREXIYCLYWSTLTLTIIIIIIIIIIIIIIIIIIIIII 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGVLIFATIVGNVGSMISNMNATRABFQAKIDAVKHYMQFRKVSKDMEAKVIKWFDYLWT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NKKTVDEREVLKNLPAKLRAEIAINVHLSTLKKVRIFQDWEAGLLVELVLKRRPQVFSPG 480
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                                                                                                                                                                                                                                                                                                                                                                                                                         Length 664;
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Pred. No. 8.6e-223m
0; Mismatches 3; Indels
               HI (POTENTIAL).

EXTRAGELLULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

H3 (POTENTIAL).

H3 (POTENTIAL).

H4 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

GYTOPLASMIC (POTENTIAL).

GYTOPLASMIC (POTENTIAL).

CAMP (BY SIMILARITY).

CAMP (POTENTIAL).

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720806950EC27F3C CRC64;
  CYTOPLASMIC (POTENTIAL).
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Matches 661; Conservative
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                                                                                                                                                                                                                                          TISSUE-Heart;
MEDLINE=5643619; PubMed=8841933;
Ruiz M.L., London B., Nadal-Ginard B.;
Ruiz M.L., London B., Nadal-Ginard B.;
Cloning and characterization of an olfactory cyclic nucleotide-gated channel expressed in mouse heart.";
J. Mol. Cell. Cardiol. 28:1453-1461(1996).
-:- FUNCTION: Odorant signal transduction is probably mediated by a G-protein coupled cascade using cAMP as second messenger. The protein coupled cascade using cAMP to be activated by cyclic nucleotides which leads to a depolarization of olfactory sensory
                                                                                                                                                                                                                                                                                                                                                                                                                      neurons.

-!- SUMICALITY: Belongs to the cyclic nucleotide-gated cation channel
- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
(TC 1.A.1.5) family.
-!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
-!- CAUTION: It is uncertain whether Met-1 or Met-2 is the initiator.
-!- CAUTION: It is uncertain whether met-1 or met-2 is the initiator.
                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
Cly-MAR-2004 (Rel. 43, Last annotation update)
Cyclic-nucleotide-gated olfactory channel (Cyclic-nucleotide-gated cation channel 2) (CNG channel 2) (CNG channel 2) (CNG channel 2) (CNG-2) (CNG-2)
                                                                                                                                     Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:108040; COGG2.

R GO; GO:0005216; F:ion channel activity; IMP.

GO; GO:0005216; F:ion channel activity; IMP.

R InterPro; IPR001525; cNMP binding.

R InterPro; IPR01525; cNMP binding.

R Pfam; PF00157; cNMP binding; 1.

R PR0517; SM01000; cNMP; 1.

R PR051TE; PS001889; CNMP BINDING 1; 1.

R PR05ITE; PS00189; CNMP BINDING 2; FALSE NEG.

R PR05ITE; PS00189; CNMP BINDING 3; 1.

R MILLIGENE FAMP BINDING 3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H2 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
H3 (POTENTIAL).
EXTRACELLUTAR (POTENTIAL).
H4 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H6 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CAMP (BY SIMILARITY).
CAMP (POTENTIAL).
CAMP (POTENTIAL).
N-LINKED (GLCNAC. .) (PC
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EXTRACELLULAR (POTENTIAL)
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 PRT;
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STANDARD;
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194
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                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Multigene family;
DOMAIN
TRANSMEM 143
                                                                                                                                                                                           NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SO QORRGGERRIVELUGVIRQWANRNEREERARPDSFLERFRGPELQIVITQQGDGKGDKDG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGKGTKKKFELFVLDPAGDWYYRWLFVIAMPVLYNWCLLVARACFSDLORNYFVVWLVLD 181
                                                                                                                                          neurons.
--- SUBCELLOLULAR LOCATION: Integral membrane protein.
--- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel (TC 1.A.1.5) family.
--- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
                  2 MTEKSNGVKSSPANNHNHHPPPSIKANGKDDHRAGSRPQSVAADDDTSPELQRLAEMDTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RRGRGGFQRIVRLVGVIRDWANKNFREEEPRPDSFLERFRGPELQTVTTHQGDDKGGKDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -LINKED (GLCNAC. . .) (POTENTIAL) 5E9170D0B322B3E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.0%; Score 3231.5; DB 1; Length 664; 93.8%; Pred. No. 2.9e-208;
                                                                                                                                                                                                                                                                                                                                                                                                         SWART; SMOOLOC COMP; 1.

PROSITE; PS00889; CNMP BINDING 1; 1.

PROSITE; PS00889; CNMP BINDING 2; 1.

PROSITE; PS50042; CNMP BINDING 3; 1.

Ionic channel; Ion transport; CAMP-binding; Transmembrane; Multigene family; Olfaction.

TRANSMEM 141 160 HI (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HI (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
H2 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
H3 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H4 (POTENTIAL).
CYTOPLASHIC (POTENTIAL).
H5 (POTENTIAL).
EXTRACELLUTAR (POTENTIAL).
H6 (POTENTIAL).
CYTOPLASHIC (POTENTIAL).
CYTOPLASHIC (POTENTIAL).
CAMP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAMP (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                          EMBL, X59668; CAA42201.1; ALT INIT.
InterPro; IPR000595; CNMP binding.
InterPro; IPR005621; Ion Trans.
InterPro; IPR005622; K+channel_pore.
Pfam; PF00027; CNMP binding; 1.
Pfam; PF00520; ion_trans; 1.
           MEDLINE=93359035; PubMed=7689061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76205 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 93.8°
Matches 622; Conservative
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1173
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1192
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2294
4453
349
664
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558
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536
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664 AA;
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                            SIGRGVDTWVYPNITDPEYGYLAREYIYCLYWSTLTLTTIGETPPPVKDBBYLFVIFDFL 360
                                                                                                                                                                                                                                                                                                        SIGEGOTWOYPNITDPEXGYLAREYIYCLYWSTLTLTTIGETPPPVKDEEYLFFIFDFL 360
                                                                                                                                                                                                                                                                                                                                                                                                 IGVLIFATIVGNVGSMISNNMATRAEFQAKIDAVKHYMQFRKVSKDMEAKVIKWFDYLWT 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DXICRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSKMGNRRTA 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        541 NIRSIGYSDLFCLSKDDLMEAVTBAPDAKKVLZERGREILMKMGLLDENFVAASWEVDVQ 600
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                                                                                                                                                                                  GEGKGTKKKFELFVLDPAGDWYKRWLFVIAMPVLYNWCLLVARACFSDLORNYFVVWLVL
                                                                                                                                                                                                      DYFSDTVYIADLIIRLRTGFLEQGLLVKDPKKLRDNYIHTLQFKLDVASIIPTDLIYFAV
                                                                            1 MMTEKSNGVKSSPANNHNHHPPPSIKANGKDDHRAGSRPQSVAADDDTSPELQRLAEMDT
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01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Cyclic-nucleotide-gated olfactory channel (Cyclic-nucleotide-gated
cation channel 2) (CNG channel 2) (CNG-2) (CNG2) (Aorta CNG channel)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryccolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Lagomorpha, Leporidae, Oryctolagus.
                                                          0
                                     97.6%; Pred. No. 1.2c=21.,
Live 3; Mismatches 13; Indels
                              Length
  90B2601D727C6AFE CRC64;
                          97.4%; Score 3384; DB 1; 97.6%; Pred. No. 1.9e-218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   664 AA
 76209 MW;
                                     al Similarity 97.6 648; Conservative
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 664 AA;
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SEQUENCE FROM N.A.
TISSUE=Aorta;
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                       Query Match
Best Local Si
Matches 648
SEQUENCE
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CNG2_RABIT
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YFSDTVYIADLIIRLRTGFLEQGLLVXDPKKLRDNYIHTLQFKLDVASIIPTDLIYFAVG 241

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 RRGRGGFQRIVRLVGVIRDWANKNFREEFPRPDSFLERFRGPELQIVTTHQGDDKGGKDG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 MTEKSNGVKSSPANNHNHHPPPSIKANGKDDHRAGSRPQSVAADDDTSPELQRLAEMDTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 EGKGTKKKPELFVLDPAGDWYYRWLFVIAMPVLYNWCLLVARACFSDLQRNYFVVWLVLD
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                                                                                                                                                                                                                                                              PEAMSTER PROSECT, ION LTALLS, T. BRANT, SMOOLOO, CANNE, I. DR SWART; SMOOLOO, CANNE, I. DR PROSITE; PSOOBBS, CNMP_BINDING_1; I. DR PROSITE; PSOOBBS, CNMP_BINDING_2; I. DR PROSITE; PSOOBBS, CNMP_BINDING_2; I. DR CANNE, PROSITE; PSOOBBS, CNMP_BINDING_3; I. DRANTSMEM 141 160 HI (POTENTIAL).

FT TRANSMEM 141 160 HI (POTENTIAL).
FT TRANSMEM 151 173 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 217 236 HI (POTENTIAL).
FT TRANSMEM 217 236 HI (POTENTIAL).
FT TRANSMEM 217 236 HI (POTENTIAL).
FT TRANSMEM 275 297 HI (POTENTIAL).
FT TRANSMEM 454 474 EVOTENTIAL).
FT TRANSMEM 454 474 EVOTENTIAL).
FT TRANSMEM 454 474 HI (POTENTIAL).
FT TRANSMEM 454 474 HI 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PROBABLE)
                                                                                                                                                                    PIR; S11521; S11521.
InterPro; IPR000595; CNMP binding.
InterPro; IPR00581; Ion Trans.
InterPro; IPR001622; K+channel_pore.
Pfam; PF00027; CNMP binding; 1.
Pfam; PF00520; ion_trans; 1.
                                                                                                                                                   EMBL; X55010; CAA38754.1; -.
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Matches 610;
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180 YFSDVVYIADLFIRLRTGFLEQGLLVKDPKKLRDNYIHTLQFKLDVASIIPTDLIYFAVG 239
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SUBCELLUCIAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Olfactory neurons.
MISSULAMPOUS: The Olfactory channel is activated by both cAMP and CGMP at similar concentrations, whereas the cGMP-gated channel is much less sensitive to CAMP.
SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
                                         IHSPEVRFNRLLHFARMFEFFDRTETRISYPNIFRISNLVLYILVIIHWNACIYYVISKS
                                                               302 IGEGUDTWVYPNITDPEYGYLAREYIYCLYWSTLTLTTIGETPPPVKDEEYLFVIFDFLI
                                                                                                                                               GVLIFATIVGNVGSMISNMMATRAEFQAKIDAVKHYMQFRKVSKDMBAKVIKWFDYLWTN
                                                                                                                                                                                                                               GVLIFATIVGNVGSMISNNNATRAEFQAKIDAVKHYMQFRKVSKEMEAKVIKWFDYLWTN
                                                                                                                                                                                                                                                                           KKTVDEREVLKOLPAKLRAEIAINVHLSTLKKVRIFQDWEAGLLVBLVLKLRPQVFSPGD
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                                                                                                                                                                                                                                                                                                                                                                               IRSLGYSDLFCLSKDDLMEAVTEAPDAXKKVLEERGREILMKMGLLDENEVAASMEVDVQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLEQLETNMDTLYTRFARLLAEYTGAQQKLKQRITVLETKMKQNHEDDYLSDGINTPEPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-MAR-2004 (Rel. 43, Last annotation update)
Cyclic-nucleotide-gated olfactory channel (Cyclic-nucleotide-gated cation channel 2) (CNG channel 2) (CNG channel 2) (CNG-2) (CNG2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    epithelium.,
FEBS Lett. 270:24-29(1990).
-!- FUNCTION: Odorant signal transduction is probably mediated
by a G-protein coupled cascade using cAMP as second messenger.
The olfactory channel can be shown to be activated by cyclic
nucleotides which leads to a depolarization of olfactory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUB=Olfactory epithelium;
MEDLINE=1022; Pubmed=1699793;
Ludwig J., Margalit T., Eismann E., Lancet D., Kaupp U.B.;
"Primary structure of cAMP-gated channel from bovine olfactory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Belongs to the cyclic nucleotide-gated catior (TC 1.A.1.5) family. SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
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                                                                                                                                                                                                                                                                                                                                          199
                                                                                                                                                                                                                            "Rod and cone photoreceptor cells express distinct genes for cGMP-gated chammels.";
Neuron 10:865-877(193).
-!- FUNCTION: Visual signal transduction is mediated by a G-protein coupled cascade using cGMP as second messenger. This protein can be activated by cyclic GMP which leads to an opening of the cation chamnel and thereby causing a depolarization of cone
KKSVDEREVLKNLPAKLRAEIAINVHLSTLKKVRIFQDCEAGLLVELVLKLRPQVFSPGD
                                                                                                    IRSLGYSDLFCLSKDDIMEAVTEAPDAKKVLEERGREILMKMGLLDENEVAASMEVDVQE
                                                                                                                                                                                                                                                                                                                      KLEQLETNMDTLYTRFARLLAEYTGAQQKLKQRITVLETKMKQNHEDDYLSDGINTEEPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauxia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Cyclic nucleotide gated channel, cone photoreceptor, alpha subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00027; CNMP Dinding; 1.

Pfam; PF00520; ion_trans; 1.

SMART; SM00100; cNMP; 1.

PROSITE; PS00889; CNMP BINDING 1; 1.

PROSITE; PS0042; CNMP BINDING 2; 1.

PROSITE; PS50042; CNMP BINDING 2; 1.

PS50042; CNMP BINDING 2; 1.

PS50042; CNMP BINDING 2; 1.

PS50042; CNMP BINDING 2; 1.

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-1- SIMILARITY: Belongs to the cyclic nucleotide-gated cation (TC 1.A.1.5) family.
-1- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=93264082; PubMed=7684234;
Boenigk W., Altenhofen W., Mueller F., Dose A., Illing M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             483 FDYLWTNKKTVDEKEVLKNLPDKLKAEIAINVHLDTLKKVRIFQDCEAGLLIELVLKKK
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                                                                                                                                                                                                          .) (POTENTIAL)
                                                                                                                                                                                                                                                                         89;
                                                                                                                                                                                                                                             63.9%; Score 2219.5; DB 1; Length 735;
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H1 (POTENTIAL).

EXTRAGELLULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

H3 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

H4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

H5 (POTENTIAL).

H6 (POTENTIAL).
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CAMP (BY SIMILARITY)
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; Mismatches 113;
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CAMP (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                  photoreceptors.
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Prominently expressed in retina.
TISSUE SPECIFICITY: Prominently expressed in retina.
SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel (TC 1.A.1.5) family.
SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Retina;
MEDLINE=20273944; PubMed=10813773;
Hirano A.A., Hack I., Waessle H., Duvoisin R.M.;
Hirano A.A., Hack I., Waessle H., Duvoisin R.M.;
"Cloning and immunocytochemical localization of a cyclic nucleotide-gated channel alpha-subunit to all cone photoreceptors in the mouse
                                                 QSUJZ8; QSWV01;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43). Last annotation update)
Cyclic-nucleotide-gated cation channel alpha 3 (CNG channel alpha photoreceptor cGNP-gated channel alpha 3) (Cone photoreceptor cGNP-gated channel alpha subunit).
                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:1341818; Cross.

R GD; GO:005221; F:intracellular cyclic nucleotide activated c. ...;

R InterPro; IPR000525; CNMP binding.

R InterPro; IPR001622; K+Channel pore.

R Pfam; PF00027; CNMP binding; 1.

R Pfam; PF00020; ion trans; 1.

R RARI; SM00100; CNMP; 1.

R RROSITE; PS00888; CNMP BINDING 1; 1.

R RROSITE; PS00889; CNMP BINDING 2; 1.

R ROSITE; PS00889; CNMP BINDING 2; 1.

R ROSITE; PS00889; CNMP BINDING 3; 1.

Innic channel; Ion transport; CAMP-binding; Transmembrane;

Multigene family; Vision.

I TRANSMEM.

ITRANSMEM.

ITRANSMEM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    send an email to license@isb-sib.ch)
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EMBL; AJ238239; CAB42891.1; --
EMBL; AJ238240; CAB42891.1; JOINED.
EMBL; AJ238241; CAB42891.1; JOINED.
                                                                                                                                                                                                                                                                                                                 Comp. Neurol. 421:80-94(2000)
                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 95-631 FROM N.A.
                                           STANDARD:
                                                                                                                                                          Mus musculus (Mouse)
                                          CNG3 MOUSE
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                RESULT 6
CNG3_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---GDDKGGKDGEGKGTKKKFELFVLDPAGDWYYRWLFVIAMPVLYNWCLLVARACFSDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QRNYFVVWLVLDYFSDTVYIADLIIRLRTGFLEQGLLVKDPKKLRDNYIHTLQFKLDVAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  470 LKLRPQVFSPGDYICRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGBISILNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3)
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01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
(Cyclic-nucleotide-gated cation channel alpha 3 (CNG 2) (Cyclic nucleotide gated channel alpha 3) (CNG 2) (Cyclic nucleotide gated channel alpha 3) (Cone photoreceptor CMP-gated channel alpha 3) (Cone CNGA3 OR CNG3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                          25;
                                                                                                                                                                                                                                                                                            Score 2151.5; DB 1; Length 631;
Pred. No. 3.5e-136;
5; Mismatches 94; Indels 25;
                                                                                                                                                                                                                            4FA8CD3B9AA3FE6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                   94;
                                                 CAMP.

CAMP (POTENTIAL).

CAMP (POTENTIAL).

C -> Y (IN REF. 2).

L -> V (IN REF. 2).
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                            POTENTIAL.
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241

301 316 361 376

421

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ISNMNATRAEFQAKIDAVKHYMQFRKVSKDMEAKVIKWFDYLWTNKKTVDEREVLKNLPA 436
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                                                      137 PAGDWYYRWLFVIAMPVLYNWCLLVARACFSDLQRNYFVVWLVLDYFSDTVYIADLIIRL
                                                                                  242 RIGFLEQGLMVMDASRLWKHYTQTLHFKLDVLSLVPTDLAYFKLGMNYPELRFNRLLKLA
                                                                                                                                                                                                                                                                                                         302 RLFEFFDRTETRINYPNMFRIGNLVLYILLIIHMNACIYFAISKFIGFGTDSWVYPNVSN
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                                                                                                                                                                RIGFLEQGLLVKDPKKLRDNYIHTLQFKLDVASIIPTDLIYFAVGIHSPEVRFNRLLHFA
                                                                                                                                                                                                                                                                         RMPEFFDRIETRISYPNIFRISNLVLYILVIIHWNACIYYVISKSIGFGVDTWVYPNITD
                                                                                                                                                                                                                                                                                                                                                                                   317 PEYGYLAREYIYCLYWSTLTLTTIGETPPPVKDEEYLFVIFDFLIGVLIFATIVGNVGSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       437 KLRAEIAINVHLSTLKKVRIFQDWEAGLLVELVLKLRPQVFSPGDYICRKGDIGKEMYII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [2]
SEQUENCE OF 320-580 FROM N.A.
MEDLINE=95175019; PubMed=732814;
Distler M., Biel M., Flockerzi V., Hofmann F.;
"Expression of cyclic nucleotide-gated cation channels in non-sensory tissues and cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CNG3 HUMAN STANDARD; PRT; 694 AA. (1652B1, COPUGE4; CONCEST, CONCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S:
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98176633; PubMed=9517456; Wissinger B., Muller F., Weyand I., Schuffenhauer S., Raupp U.B., Zrenner B.; "Cloning, chromosomal localization and functional expresence encoding the alpha-subunit of the cGMP-gated chan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         662 RFARLLAEYNATQMKVKQRLSQLESQVKMGLPPD 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          616 RFARLLAEYTGAQQKLKQRITVLETKMKQNHEDD
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J. Neurosci. 9:2512-2521(1997)
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MEDLINE=98324775; PubMed=9662398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                 Biel M., Zong X., Distler M., Boëse E., Klugbauer N., Murakami M., Flockerzi V., Hofmann F.; Flockerzi V., Hofmann F.; "Another member of the cyclic nucleotide-gated channel family, expressed in testis, kidney, and heart."; Proc. Natl. Acad. Sci. U.S.A. 31.3505-3509(1994).

-!- FUNCTION: Could be responsible for cGMP-induced calcium entry in cells other than sensory cells. Might be involved in chemotaxis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----GKGTKKKFELFVLD
                                             TISSUE=Testis;
MEDLINE=94211295; PubMed=7512693;
Weyand I., Godde M., Frings S., Weiner J., Mueller F., Altenhofen W.,
Hatt H., Kaupp U.B.;
"Cloning and functional expression of a cyclic-nucleotide-gated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Testis, kidney, retinal cone and heart.
SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
(TC 1.A.1.5) family.
SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSPANNHNHHPPPSIKANGKD-DHRAGSRPQSVAADDDTSPELQRLAEMDTPRRGRG---
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PROSITE; PS00889; CNMP BINDING 2; 1.
PROSITE; PS0042; CNMP BINDING 3; 1.
IONIC channel; Ion transport; CAMP-binding; Transmembrane; Miltigene family; Vision.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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; Pred. No. 2.4e-135;
94; Mismatches 119;
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InterPro; IPR00595; CNMP_binding.
InterPro; IPR05821; Ion trans.
InterPro; IPR01622; K+channel_pore.
Pfam; PF00027; CNMP_binding; 1.
Pfam; PF00520; ion_trans; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAMP.
                                                                                                                                                                                                                                                                                           TISSUE=Kidney;
MEDLINE=94224768; PubMed=8170936;
                                                                                                                                                                                 channel from mammalian sperm.";
Nature 368:859-863(1994).
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60.4%;
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706 AA;
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Apfelstedt-Sylla B., Zrenner B., Sharpe L., Wissinger B.; "Total colourblindness is caused by mutations in the gene encoding the alpha-subunit of the cone photoreceptor CGMP-gated cation channel."; Nat. Genet. 19:257-259[1998].
                                                                                     -!- FUNCTION: Visual signal transduction is mediated by a G-protein coupled cascade using cGMP as second messenger. This protein can be activated by cyclic GMP which leads to an opening of the cation channel and thereby causing a depolarization of cone
                                                                                                                                              photoreceptors.
SUBCELUILAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Prominently expressed in retina.
DISEASE: Defects in CNGA3 are a cause of rod monochromacy (RMCH)
[MIM:216900]; also known as total colorblindness or achromatopsia.
RMCH is an autosomal recessively inherited condition.
SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel (TC 1.A.1.5) family.
SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
DATABASE: NAME-Autations of the CNGA3 gene;
NOTE-Retina International's Scientific Newsletter;
WWW="http://www.retina-international.com/sci-news/cnga3mut.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00889; CNMP_BINDING_1; 1.
PROSITE; PS00889; CNMP_BINDING_2; 1.
PROSITE; PS50042; CNMP_BINDING_3; 1.
Ionic channel; Ion transport; CAMP-binding; Transmembrane;
Multigene 171 192 POTENTIAL.
TRANSMEM 171 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activity; TAS
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/FTId=VAR 010906.
R -> W (in RMCH).
/FTId=VAR 010910.
V -> M (in RMCH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T -> M.
/FTId=VAR_010902.
P -> L (in RMCH).
/FTId=VAR_010903.
R -> Q (in RMCH).
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F -> L (in RMCH)
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/FTId=VAR 010904
R -> W (in RMCH)
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PIR, 178560, 178560.
Genew, HGNC:2150, CNGA3.
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                                                                                                                                                                                                                                                                                                                                                                                                                     56 GLADSGQGSFTGQGIARLSRLIFLLRRWAARHVHHQDQGPDSFPDRFRGAELKEVSSQBS 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295 TNYPNMFRIGNLVLYILLIIHWNACIYFALSKFIGFGTDSWVYPNISIPEHGRLSRKYIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       355 SLYWSTLTLTTIGETPPPVKDEEYLFVVVDFLVGVLIFATIVGNVGSMISNWMASRAEFQ
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                                                                                                                                                                                                                                                       5 KSNGVKSSPANNHNHHPPPSIKANGKDDHRAG---SRPQSVAADDDTSPBLQRLAEMDT-
                                                                                                                                                                                        Gaps
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
Ictaluridae; Ictalurus.
                                                                                                                                                                                           46;
                                                                                                                             Length 694;
                                                                                                                                                                                        Indels
557 G -> R (in RMCH).
/FTIG=VAR 010909.
78838 MW; AE00B4EE760D70A0 CRC64;
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                                                                                                                          61.6%; Score 2139; DB 1; 61.5%; Pred. No. 2.7e-135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     628 QOKLKORITVLETKMKONHEDDYLSDGINTPEPTAAE
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01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
Ictalic nucleotide-gated cation channel.
Ictalurus punctatus (Channel catfish).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               682 AA
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TISSUE=Olfactory neuroepithelium;
                                                                                                                                                                                        429; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 D----DKG-
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         557
                                                                 694 AA;
                                                                                                                                                           Similarity
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         557
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P55934;
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                                                                 SEQUENCE
                                                                                                                             Query Match
                                                                                                                                                              Best Local
         VARIANT
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TETRISYPNIFRISHLVLYILVIIHWNACIYYVISKSIGFGVDTWVYPNITDPEYGYLAR 324
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PIR; I50680; I50680.
InterPro; IPR00595; CNMP binding.
InterPro; IPR005821; IOn_Erans.
                                                                                                                                                                                                                                                                                                                                                                                                                  624 YIGAQQKLKQRITVLETKM 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                   634
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SEQUENCE FROM N.A.
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CNG3_CHICK
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                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                       REBL; M83111; -; NOT_ANNOTATED_CDS.
R PIR; JH0560; JH0560.
R InterPro; IPR000595; CMMP_binding.
R InterPro; IPR001621; K+channel_pore.
R InterPro; IPR001201; PAP 25A core.
R InterPro; IPR001201; PAP 25A core.
R Flam; PF00220; ion trans; 1.
R Pfam; PF00820; ion trans; 1.
R PROSITE; PS00889; CMMP_BINDING_1; 1.
R PROSITE; PS00889; CMMP_BINDING_2; 1.
R PROSITE; PS00842; CMMP_BINDING_2; 1.
R PROSITE; PS0042; CMMP_BINDING_3; 1.
M Olfaction; Ion transport; Ionic channel; CAMP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 VETEQRPDSFLERFRGPQ-----AANDQSAAPADAPKKTFKERWEGFVVSQSDDIYYY
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Pred. No. 9.1e-135;
68; Mismatches 110; Indels
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CYTOPLASMIC (POTENTIAL).
H3 (POTENTIAL).
H4 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CAMP (BY SIMILARITY).
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 MEDLINE=92110008; PubMed=1370374;
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529
682 AA;
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Best Local Similarity
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219
240
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                                                                                                                                                          316 CYVYCEYWSTLILITIGEMPPPVXDEEYVFVVFDFLVGVLIFATIVGNVGSMIANMAIR 375
                                                                                                                                                                                                                                                                                  444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  436 NVHLDTLKKVRIFQDCEAGLLVELVLKLRPQVYSPGDYICKKGDIGKEMYIIKEGQLAVV 495
                                                                                                          384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDGVTQYALLSAGSCFGEISILNIKGSKMGNRRTANIRSLGYSDLFCLSKDDLMEAVTE 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        565 APDAKKVLEERGREILMKMGLLDENEVAASMEV-DVQEKLEQLETNMDTLYTRFARLLAE 623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 NVHLSTLKKVRIFQDWEAGLLVELVLKLRPQVFSPGDYICRKGDIGKEMYIIKEGKLAVV
TETRINYPNAFRICNLILYILVIIHWNACIYXAISKALGLSSDTWVYSG----QNKTLSF
                                                                                                                                                                                                                                                                                                                              ADDGVTQFALLTAGGCFGEISILNIQGSKMGNRRTANIRSIGYSDLFCLSKDDLMEAVAE
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-!- SMILARITY: Belongs to the cyclic nucleotide-gated cation channel (TC 1.A.1.5) family.
-!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
                                                                                                          325 EYIYCLYWSTLTLTTIGETPPPVKDEEYLFVIFDFLIGVLIFATIVGNVGSMISNMNATR
                                                                                                                                                                                                                                                                                  AEFQAKIDAVKHYMQFRKVSKDMEAKVIKWFDYLWTNKKTVDEREVLKNLPAKLRAEIAI
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NAR-2004 (Rel. 43, Last annotation update)
Cyclic nucleotide gated channel, ROD photoreceptor, alpha subunit (CNG channel 3) (CNG-3) (CNG-3)
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Boenigk W., Altenhofen W., Mueller F., Dose A., Illing M.,
Molday R.S., Kaupp U.B.;
"Rod and cone photoreceptor cells express distinct genes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         645 AA.
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BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IADLIIRLRIGFLEQGLLVKDPKKLRDNYIHTLQFKLDVASIIPTDLIYFAVGIHSPEVR 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HHPPPSIKANGKDDHRAGSRPQSVAADDDTSPELQRLAEMDTPRRGRGGFQRIVRLVGVI 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HHSHPII------PSVVVQDTSEDPGL----IEKGENRFARQWYLPGAF 47
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                                                                                      PROSITE; PS00888; CNMP_BINDING_1; 1.
PROSITE; PS00889; CNMP_BINDING_2; 1.
PROSITE; PS50042; CNMP_BINDING_3; 1.
Ionic channel; Ion transport; GAMP-binding; Transmembrane; Vision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.5%; Score 2067; DB 1; Length 645; 62.9%; Pred. No. 1.6e-130; ive 78; Mismatches 123; Indels 38
                                                                                                                                                                                                                                                                                                                  H3 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
H4 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
H6 (POTENTIAL).
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74778 MW; 989D515F61AC7D31 CRC64;
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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                     Pfam; PF00027; cNMP_binding;
Pfam; PF00520; ion_frans; 1.
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                                                                                                                                                                       01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-MAR-2004 (Rel. 24, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
60MP-gated cation channel alpha 1 (CNG channel alpha 1) (CNG-1) (CNGI)
(Cyclic nucleotide gated channel alpha 1) (Cyclic nucleotide gated channel, photoreceptor (Cyclic-nucleotide-gated cation channel 1)
(Rod photoreceptor cGMP-gated channel alpha subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92112723; PubMed=1370452; Wohlfart P., Haase W., Molday R.S., Cook N.J.; Manale W., Molday R.S., Cook N.J.; Manale Sanday R.S., Sanday R.S., Gook N.J.; Mattibodies against synthetic peptides used to determine the topology and site of glycosylation of the cGMP-gated channel from bovine rod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: Fomotetramer or higher oligomer.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BOLORTICITY: Rod cells in the retina.
-!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel (TC 1.A.1.5) family.
-!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
TISSUB-Retinal rod cell;
MEDLINE-9008076; Pubmed=2481236;
Kaupp U.B., Niidome T., Tanabe T., Terada S., Boenigk W.,
Stuehmer W., Cook N.J., Kangawa K., Matsuo H., Hirose T., Miyata T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7. Biol. Chem. 267:644-648 (1992).
-!-FUNCTION: Visual signal transduction is mediated by a G-protein coupled cascade using cGMP as second messenger. This protein can be activated by cGMP which leads to an opening of the cation channel and thereby causing a depolarization of rod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92255398; PubMed=1316156;
Kumar V.D., Weber I.T.;
"Molecular model of the cyclic GMP-binding domain of the cyclic GMP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Primary structure and functional expression from complementary DNA of the rod photoreceptor cyclic GMP-gated channel."; Nature 342:762-766(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95365381; PubMed=7543681;
Henn D.K., Baumann A., Kaupp U.B.;
"Probing the transmembrane topology of cyclic nucleotide-gated ion channels with a gene fusion approach.";
Proc. Natl. Acad. Sci. U.S.A. 92:7425-7429(1995).
                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                        627
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                                                                                                                                   069
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                                                                                                                                   STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                            Bovidae, Bovinae, Bos.
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P2973; Q16279; Q16485; Created)
01-APR-1993 (Rel. 25, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
GMP-gated cation channel alpha 1 (CNG channel alpha 1) (CNG-1) (CNG1)
C(Cyclic nucleotide gated channel alpha 1) (Cyclic nucleotide gated channel, photoreceptor (Gyclic-nucleotide-gated cation channel 1)
(Rod photoreceptor cGMP-gated channel alpha subunit).
CNG1 OR CNG3 OR CNGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WEDLINE=96036047; PubMed=7479749;
MEDLINE=96036047; PubMed=7479749;
MEDLINE=96036047; PubMed=7479749;
Mutations in the gene encoding the alpha subunit of the rod cGMP-gated channel in autosomal recessive retinitis pigmentosa.";
Proc. Natl. Acad. Sci. U.S.A. 92:10177-10181 (1995).
-!- FUNCTION: YISUAL SIGNAL TRANSDUCTION IS MEDIATED BY A G-PROTEIN ES ACTIVATED BY COUPLED CASCADE USING CRAP AS SECOND MESSENGER. THIS PROTEIN COUPLED CASCADE USING CAMP AS SECOND MESSENGER. THIS PROTEIN CAN BE ACTIVATED BY CYCLIC GMP WHICH LEADS TO AN OPENING OF THE CATION CHANNEL AND THEREBY CAUSING A DEPOLARIZATION OF ROD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      leads to degeneration of retinal photoreceptor cells.
SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
(TC 1.A.1.5) family.
SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
DATABASE: NAWE-Mutations of the CNGAl gene;
NOTE-Retina International's Scientific Newsletter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     channels in non-sensory
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TISSUB SPECIFICITY: Rod cells in the rethins.
DISEASE: Defects in COA1 are a cause of autosomal recessive retinitis pigmentosa (ARRP) [MIM:123825]. ARRP is a disease that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Homotetramer or higher oligomer. Forms heterooligomeric complex with CNG4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Retina;
MEDLINE-92210603; PubMed=1372902;
MEDLINE-92210603; PubMed=1372902;
Bittler S.J., Lee A.K., Jtherr M.R., Howard T.A., Seldin M.F.,
Hurwitz R.L., Masmuth J., Baehr W.;
"Primary structure and chromosomal localization of human and mouse rod photoreceptor cGMP-gated cation channel.";
J. Biol. Chem. 267:6257-6262(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUB=Retina;
Macke J.P., Eddy R.L., Shows T.B., Reed R.R.,
Dhallan R.S., Macke J.P., Eddy R.L., Shows T.B., Reed R.R.,
Yau K.-W., Nathans J.;
Human rod photoreceptor cGMP-gated channel: amino acid sequence,
gene atructure, and functional expression.";
J. Neurosci. 12:3248-3256(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95175019; PubMed=7532814;
Distler M., Balel M., Flockerzi V., Hofmann F.;
Expression of cyclic nucleotide-gated cation c
tissues and cells.";
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                                                                                                                                                                                                            686 AA
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                                                                                                                                                                                                            STANDARD;
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               PIR, S07103; S07103.

InterPro; IPR00595; CNMP binding.
InterPro; IPR005821; Cno trans.
InterPro; IPR001821; K+channel_pore.
Pfam; PF001027; CNMP binding; 1.
Pfam; PF00100; CNMP binding; 1.
SMART; SM00100; CNMP 1.
PROSITE; PS00888; CNMP BINDING 1; 1.
PROSITE; PS000889; CNMP BINDING 2; 1.
PROSITE; PS000889; CNMP BINDING 3; 1.
IONIC channel; Ion transport; CGMP-binding; Transmembrane; Multigene family; Vision.
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A01CFB6567424455 CRC64;
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CYTOPLASMIC (PROBABLE).
H3 (PROBABLE).
EXTRACELLULAR (PROBABLE).
CYTOPLASMIC (PROBABLE).
CYTOPLASMIC (PROBABLE).
H5 (PROBABLE).
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H7 (PROBABLE)
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GKDGEGKGTKKKFELFVLDPAGDWYYRWLFVIAMPVLYNWCLLVARACFSDLORNYFVVW 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Sprague-Dawley;
MEDLINE=97197878; PubMed=9045728;
Bradley J., Zhang Y., Bakin R., Lester H.A., Ronnett G.V., Zinn K.;
"Functional expression of the heteromeric 'olfactory' cyclic
nucleotide- gated channel in the hippocampus: a potential effector of synaptic plasticity in brain neurons.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  497 SPGDYICKKGDIGREMYIIKEGKLAVVADDGVTQFVVLSDGSYFGEISILNIKGSKAGNR
                        137 EEKSKOKKEEEKKEVVVIDPSGNTYYNWLFCITLPVMYNWTWVIARACFDELQSDYLEYW
                                                                                              377 DFLIGVLIFATIVGNIGSMISNMNAARAEFQARIDAIKQYMHFRNVSKDMEKRVIKWFDY
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                                                                          LVLDYFSDTVYIADLIIRLRIGFLEQGLLVKDPKKLRDNYIHTLQFKLDVASIIPTDLIY
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Ebkaryota; Metazoa (rat).
Bukaryota; Metazoa (Chordata; Craniata; Vertebrata; Buteleostomi;
Ammanlia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDLINE=97287732; PubMed=9142860;
Ding C., Potter E.D., Qiu W., Coon S.L., Levine M.A., Guggino S.E.;
"Cloning and widespread distribution of the rat rod-type cyclic
nucleotide-gated cation channel.";
Am. J. Physiol. 272:C1335-C1344(1997).
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Barnstable C.J., Wei J.Y.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
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                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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  WWW="http://www.retina-international.com/sci-news/cngalmut.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                MIN, 123825.

MIN, 122825.

GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0006810; P:transport; TAS.
GO; GO:0006011; P:transport; TAS.
InterPro; IPRO0595; cNMP_binding.
InterPro; IPRO05821; Ion_trans.
InterPro; IPRO0522; K-frannel_pore.
Fram; PRO0520; con_trans; 1.
Fransmembrane; PROSITE; PS00889; cNMP_BINDING_2; 1.
FROSITE; PS00889; cNMP_BINDING_2; 1.
FROSITE; PS00889; cNMP_BINDING_2; 1.
FROSITE; PS00889; cNMP_BINDING_3; 1.
Ionic channel; Ion transport; GGMP-binding; Transmembrane; Multigene family; Vision; Disease mutation; Polymorphism; PROSITE; PS0042; CMP-binding; Transmembrane; Multigene family; Vision; Disease mutation; Polymorphism; PROSITE; PS0042; CMP-binding; Transmembrane; PROSITE; PS042042; CMP-binding; Transmembrane; PROSITE;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.5%; Score 2034; DB 1; Length 6 61.4%; Pred. No. 2.7e-128; ive 88; Mismatches 135; Indels
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
H6 (POTENTIAL).
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H3 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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/FIXES-NA 009297.

S -> Y (IN REF. 1).

L -> I (IN REF. 1).

RE -> HH (IN REF. 1).

GA -> WS (IN REF. 1).

GA -> WS (IN REF. 1).
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/FTId=VAR 009296
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Best Local Similarity 61.4%;
Matches 403; Conservative 8
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Genew, HGNC:2148; CNGA1.
MIM; 123825;
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686 AA;
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547 KAGNRRTANIKSIGYSDLFCLSKDDLMEALTEYPDAKTWLEEKGRQILMKDGLLDINIAN
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173 YFVVWLVLDYFSDTVYIADLIIRLRIGFLEQGLLVKDPKKLRDNYIHTLQFKLDVASIIP
                         187 YLEYWLIFDYVSDVVYLADMFVRTRTGYLEQGLLVKDELKLIEKYKANLQFKLDVLSVIP
                                                   TDLIYFAVGIHSPEVRFNRLLHFARMFEFFDRTETRTSYPNIFRISNLVLYILVIHWNA
                                                                 247 TDLLYFKFGWNYPEIRLNRLERISRMFEBFQRTETRTNYFNIFRISNLVMYIVIIHWNA
                                                                                                     CIYYVISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWSTLTLTIGETPPPVKDEEY
                                                                                                                    KWFDYLWTNKKTVDEREVLKNLPAKLRAEIAINVHLSTLKKVRIFQDWEAGLLVELVLKL
                                                                                                                                                                                                                                     427 KWEDYLWINKKTVDEREVLRYLPDKLRAEIAINVHLDTLKKVRIFADCEAGLLVELVLKI
                                                                                                                                                                                                                                                                                                                    KMGNRRTANIRSLGYSDLFCLSKDDLMEAVTEAPDAKKVLEERGREILMKMGLLDENEV-
                                                                                                                                                                                                                                                                                                                                                                         592 AASMEVDVQEKLEQLETNMDTLYTRFARLLAEYTGAQQKLKQRITVLETKMKQNHEDDY-
                                                                                                                                                          LFVIFDFLIGVLIFATIVGNVGSMISNMNATRAEFQAKIDAVKHYMQFRKVSKDMBAKVI
                                                                                                                                                                                                                                                                  RPQVFSPGDYICRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGZISILNIKGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: Homotetramer or higher oligomer. SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       691 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                              -LSDGINTPEPT 661
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STRAIN=Beagle X Briard;
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Q28279;
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                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 GFQRIVRLVGV----IRDWANKN-----FREEEPRPDSFLERFRGPELQTVTTHQ 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 NGACSSFSDNDN----SNSYRRG 66
           FUNCTION: VISUAL SIGNAL TRANSDUCTION IS MEDIATED BY A G-PROTEIN COUPLED CASCADE USING CGMP AS SECOND MESSENGER. THIS PROTEIN CAN BE ACTIVATED BY CYCLIC GMP WHICH LEADS TO AN OPENING OF THE CATION PHOTORECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NGVKSSPANNHNHHPPPSIKANGKDDHRAGSRPQSVAADDDTSPELQRLAEMDTPRRGRG
                                                                           SUBUNIT: Homoretramer or higher oligomer.
SUBCELLULAR LOCATION: Integral membrane protein.
SISUE SPECIFICITY: Rod cells in the retina.
SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel (TC 1.8.1.5) family.
SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .) (POTENTIAL)
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                                                                                                                                                                                                                                                                           EMBL; U48803; AAA92110.1; -.
EMBL; U98851; AAC53139.1; -.
EMBL; U98851; AAC57594.1; -.
EMBL; U76220; AAC17594.1; -.
InterPro; IPR000592; cNMP binding.
InterPro; IPR001622; K+channel_pore.
Ffam; PF00027; cNMP_binding; 1.
Ffam; PF00020; ion_trans; 1.
SWART; SM00100; cNMP; 1.
FFAMI; PS00888; CNMP_BINDING_2; 1.
FROSITE; PS00888; CNMP_BINDING_2; 1.
FROSITE; PS00889; CNMP_BINDING_2; 1.
FROSITE; PS00642; CNMP_BINDING_3; 1.
FROSITE; PS00642; CNMP_BINDING_3; 1.
FROSITE; PS00642; CNMP_BINDING_3; 1.
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91; Mismatches 136; Indels
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EXTRACELLULAR (POTENTIAL).

H4 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

H5 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
CGMP (POTENTIAL).
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CGMP (POTENTIAL).
N-LINKED (GLONAC. . .)
IN -> KV (IN REF. 2).
E -> G (IN REF. 2).
E -> K (IN REF. 2).
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Neurosci. 17:1993-2005(1997)
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683 AA;
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650

546

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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
115-WAR-2004 (Rel. 43, Last annotation update)
cGMP-gated cation channel alpha 1 (CNG channel alpha 1) (CNG-1) (CNG1)
(Cyclic nucleotide gated channel alpha 1) (Cyclic nucleotide gated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eye Res. 65:301-309(1997). FUNCTION: Visual signal transduction is mediated by a G-protein coupled cascade using CGMP as second messenger. This protein can be activated by CGMP which leads to an opening of the cation channel and thereby causing a depolarization of rod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECUENCE FROM N.A. MEDINEG=9268598; Charles 9415722; PubMed=9268598; Chang Q., Pearce-Kelling S., Acland G.M., Aguirre G.D., Ray K.; Canine rod photoreceptor cGMP-gated channel protein alpha-subunit: studies on the expression of the gene and characterization of the
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                           channel, photoreceptor) (Cyclic-nucleotide-gated cation channel (Rod photoreceptor cGMP-gated channel alpha subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
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NCBI TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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356
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                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VWLVLDYFSDTVYIADLIIRLRIGFLEQGLLVKDPKKLRDNYIHTLQFKLDVASIIPTDL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198 YWIIFDYLSDIVYLLDMFVRTRTGYLEGGLLVREEAKLIEKYKSNLQFKLDFLSVIPTDL 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IYFAVGIHSPEVRFNRLLHFARMFEFFDRTETRTSYPNIFRISNLVLYILVIIHWNACIY 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQYLPGAIALFUVNNSSNKEOBPKEKKKKKKKKKKKKKGDXNENKKDSEKKKKKKEKEKEKK 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSIKANGKDDHRAGSRPQSVAAD---DDTSPELQRLAEMDTPR------RGRGGFQR 70
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to the cyclic nucleotide-gated cation channel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 691;
           (TC 1.A.1.5) family.
-!- SIMILARITY: Contains 1 cyclic nuclectide-binding domain.
                                                                                                                                                                                                                         Score 2017.5; DB 1; Length; Pred. No. 3.5e-127; 94; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
H3 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .DINKED (GLCNAC. . .) (F) 0775CAA42F065275 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
HS (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
H6 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                            PIR, JC6509; JC6509.
InterPro; IRR000595; CMP binding.
InterPro; IPR001582; Ion Trans.
InterPro; IPR001622; K+channel pore.
Fran; PF00021; CMP binding; 1.
Fran; PF00520; ion trans; 1.
SMART; SM00100; cMPP; 1.
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61.3%;
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                                                                                                                                                    U83905; AAB61707.1;
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398; Conserv
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                                                                                                                       438 DYLWTWKKTVDEKEVLKYLPDKLRAEIAINVHLDTLKKVRIFADCEAGLLVELVLKLQPQ 497
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  415
                                            437
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01-APR-1993 (Rel. 25, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
GCMP-gated cation channel alpha 1 (CNG channel alpha 1) (CYGlic nucleotide gated channel, photoreceptor) (Cyclic-nucleotide-gated cation channel, photoreceptor) (Cyclic-nucleotide-gated cation channel 1)
(Rod photoreceptor) (Cyclic-nucleotide-gated cation channel 1)
(Rod photoreceptor) (Cyclic-nucleotide-gated cation channel 1)
(Rod photoreceptor) (CYClic-nucleotide-gated cation channel 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      medullary collecting duct.";
Blochim. Biophys. Acta 1236:197-200(1995).
-!- FUNCTION: VISUAL SIGNAL TRANSDUCTION IS MEDIATED BY A G-PROTEIN COUPLED CASCADE USING CGMP AS SECOND MESSENGER. THIS PROTEIN CAN BE ACTIVATED BY CYCLIC GMP WHICH LEADS TO AN OPENING OF THE CATION CHANNEL AND THEREBY CAUSING A DEPOLARIZATION OF ROD PHOTORECEPTORS.
                                                                                                                                                                                        VFSPGDYICRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSKMG
                                                                                                                                                                                                                 498 VYSPGDYICKKGDIGREMYIIKEGKLAVVADDGITQFVVLSDGSYFGEISILNIKGSKAG
                                                                                                                                                                                                                                                                                  536 NRRIANIRSLGYSDLFCLSKDDLMEAVTEAPDAKKVLEERGREILMKMGLLDENEV-AAS
                                                                                                                                                                                                                                                                                                                558 NRRTANIKSIGYSDLFCLSKDDLMEALTEYPDAKTWLEEKGKQILMKDGLLDINIANAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel (TC 1.A.1.5) family.
                           . VVDFLIGVLIFATIVGNIGSMISNMAARAEFQARIDAIKQYMHFRNVSKDMEKRVIKWF
IFDFLIGVLIFATIVGNVGSMISNMNATRAEFQAKIDAVKHYMQFRKVSKDMEAKVIKWF
                                                                                            DYLWINKKIVDEREVLKNLPAKLRAEIAINVHLSTLKKVRIFQDWEAGLLVELVLKKRPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBDATT: Homotetramer or higher oligomer.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Rod cells in the retina and inner medulla of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Retina;
MDDLNE=-S210663; PubMed=1372902;
MDDLNE=-S210663; PubMed=1372902;
Bachr W., Waguth J.J., Hurwitz R.L., Seldin M.F., Howard T.A.,
Altherr M.R., Lee A.K., Pittler S.J.;
Altherr M.R., Lee A.K., Pittler S.J.;
"Primary structure and chromosomal localization of human and mouse
"Primary structure cGMP-gated capted channel.";
J. Biol. Chem. 267:6257-6262(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a cGMP-gated cation channel from mouse kidney inner
                                                                                                                                                                                                                                                                                                                                                                                 643
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Karlson K.H., Ciampolillo-Bates F., McCoy D.B., Kizer N.L.,
                                                                                                                                                                                                                                                                                                                                                                                 595 MEVDVQEKLEQLETNMDTLYTRFARLLAEYTGAQQKLKQRITVLETKMK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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9
    (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 PNVIVPAIEKEIRRMENGACSSFSDDDNGSLSEESENEDSFFRSNSYKRRGPSQREQHLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. . .) (POTENTIAL).
NK -> I (IN REF. 1).
D -> N (IN REF. 1).
A -> V (IN REF. 1).
R -> C (IN REF. 1).
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                                                                                                                                              MGD; MGI 88436; CORGINAL SINGLES SINGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELULAR (POTENTIAL).

EXTRACELULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

H5 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

H6 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CGMP (POTENTIAL).

CGMP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                           H1 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
H2 (POTENTIAL).
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entities requires a license agreement ( or send an email to license@isb-sib.ch)
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                                                              EMBL; M84742; AAA37425.1; -. EMBL; U19717; AAA85702.1; -. EMBL; U19715; AAA85700.1; -. EMBL; U19716; AAA85701.1; -.
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                 435 TNKKTVDEREVLRYLPDKLRAEIAINVHLDTLKKVRIFADCEAGLLVELVLKLQPQVYSP
                                                                 GDYICRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSKMGNRRT
                                                                                   495 GDYICKKGDIGREMYIIKEGKLAVVADDGITQFVVLSDGSYFGEISIINIKGSKRGNRRT
                                                                                                                                   540 ANIRSLGYSDLFCLSKDDLMEAVTEAPDAKKVLEERGREILMKMGLLDENEV-AASMEVD
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Search completed: May 12, 2004, 11:14:14 Job time : 19 secs

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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Q80xh6 mus musculu		Q9er32 rattus norv	Q9er33 rattus norv	Q9qwn7 rattus norv	Q9n0h4 sus scrofa	Q804i6 carassius a	Q8uvt8 oncorhynchu	Q8jfp0 ictalurus p	Q8jfn9 ictalurus p	Q8iv77 homo sapien	lod sulumil 611260	Q9w201 drosophila	Q9qx26 rattus norv	Q9u5e2 drosophila	Q8ir35 drosophila
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		Score	3405	2160.5	2147.5	2140	2132	2035	1927	1862	1433	1375	1278.5	1180.5	1176	1128	1068	166
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ALIGNMENTS

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                                                                                                                                                                                                                                                  1 MMTEKSNGVKSSPANNHNHHPPPSIKANGKDDHRAGSRPQSVAADDDTSPELQRLAEMDT
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A Strausberg R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
R EMBL; BC048775; AAH48775.1.
R GO; GO:0016020; C::membrane; IEA.
R GO; GO:0005216; F:ion channel activity; IEA.
R GO; GO:0006811; P:ion transport; IEA.
R InterPro; IPR001652; CAMP_binding.
R InterPro; IPR001652; K+dhannel_pore.
DR Pfam; PF00520; ion trans; 1.
DR SWART; SW00100; cAMP; 1.
DR SWART; SW00100; cAMP; 1.
DR PROSITE; PS00889; CAMP_BINDING_1; 1.
DR PROSITE; PS00889; CAMP_BINDING_2; 1.
DR PROSITE; PS00889; CAMP_BINDING_2; 1.
DR PROSITE; PS00889; CAMP_BINDING_3; 1.
                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                        Query Match

98.0%; Score 3405; DB 11;
Best Local Similarity 98.2%; Pred. No. 6.5e-244;
Matches 652; Conservative 3; Mismatches 9;
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TISSUB-EBYE;

WEDLINE-22388257; PubMed=12477932;

KETAUSDERG R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RITAUSDERG R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RIAUSDERG R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RIAUSDERG R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A loghins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh F.,

A promstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley K.C., Hale S., Garcia M. M., Gay L.J., Hulyk S.W.,

Richards S. Worley K.C., Hale S., Garcia R. W., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia R.D., Lu X., Gibbs R.A.,

Rahesiley R.W., Touchman J.W., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Ratesiley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R rzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

R Generation and initial analysis of more than 15,000 full-length human
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Strausberg R.,
Submitted (MAR-2003) to the EMBL/Genbank/DDBJ databases.
B Submitted (MAR-2003) to the EMBL/Genbank/DDBJ databases.
R REMBL; BC035272; AAH49145.1; -.
R RMBL; PC0534; PT0534.
R RMBL; PC0524; PT0534.
R RGC) GO:005221; F:intracellular cyclic nucleotide activated and rerpro; IPR00595; cNMP binding.
InterPro; IPR00595; cNMP binding.
R InterPro; IPR00595; cNMP binding.
R Refero; IPR00612; K+channel_pore.
R Refero; IPR001002; K+channel_pore.
R Refero; IPR001002; K+channel_pore.
R RART; SM00100; cNMP binding; 1.
R RART; SM00100; cNMP BINDING 1; 1.
R ROSITE; PS00889; CNMP BINDING 2; 1.
R ROSITE; PS00889; CNMP BINDING 3; 1.
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                                                                                   Last sequence update)
Last annotation update)
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Æ
                                                          Created)
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                                                    01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25, Hypothetical protein (Cnga3
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PRELIMINARY;
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407; Conservative
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                                                                             EEYLFVIFDFLIGVLIFATIVGNVGSMISNMNATRAEFQAKIDAVKHYMQFRKVSKDMEA 409
                                                                                      KVIKWFDYLWINKKIVDEREVLKNLPAKLRAEIAINVHLSTLKKVRIFQDWEAGLLVELV 469
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                                                                                                                                                          KGSKMGNRRTANIRSLGYSDLFCLSXDDLMEAVTEAPDAKKVLEERGREILMKMGLLDEN 589
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                                                                                                                                                                                                                                                                                                                                                                           Kattus Morvegitus (Kat.).
Eukaryota, Metazoa (Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Rattus.
                  WNACIYFAISKFIGFGTDSWVYPNTSKPEYARLSRKYIYSLYMSTLTLTTIGETPPPVKD
                                                                                                                         LKLRPQVFSPGDYICRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNI
         IIPTOLIYFAVGIHSPEVRFNRLLHFARMFEFFDRTETRTSYPNIFRISNLVLYILVIIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 2147.5; DB 11; Length 632; Pred. No. 1.2e-150;
                                            WNACIYYVISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWSTLTI
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Last annotation update)
                                                                                                                                                                                                                                                                                                                   632
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PROSITE; PS00889; CNMP BINDING 1; 1.
PROSITE; PS00889; CNMP BINDING 2; 1.
PROSITE; PS50042; CNMP BINDING 3; 1.
                                                                                                                                                                                                                                                                                                                                    Created)
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01-MAR-2001 (TrEMBLrel. 16, Last sec
01-UUN-2003 (TrEMBLrel. 24, Last ann
Cyclic nuclectide-gated channel 2a.
Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                  PRT;
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64.5%;
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Best Local Similarity

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1]

WE SEQUENCE FROM N.A.

AS GENERALE FROM N.A.

WEDLINE=2044421; PubMed=10984544;

AN MEDLINE=2044421; PubMed=10984544;

AN MEDLINE=20442421; PubMed=10984544;

AN GGMP-Signalling pathway in a subset of olfactory sensory neurons.";

R. A. GGMP-Signalling pathway in a subset of olfactory sensory neurons.";

R. A. GGMP-Signalling pathway in a subset of olfactory sensory neurons.";

R. BREL; AJZ12428; CAC09430.1; ---

DR GO; GO:0005216; Frion channel activity; IEA.

BR GO; GO:0006216; Frion channel activity; IEA.

BR GO; GO:0006811; Prion transport; IEA.

DR GO; GO:0006811; Prion transport; IEA.

BR GO; GO:0006813; Priotassium ion transport; IEA.

DR GO; GO:0006813; Priotassium ion transport; IEA.

BR GO; GO:0006813; Priotassium ion transport; IEA.
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                                                                                                                                                                                                                                                                                                                                                            274 IFRISNLVLYILVIIHWNACIYYVISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWS
                                                                                                                                                                                                                                                                                                                                                                                                                                            334 TLTLTTIGETPPPVKDEEYLFVIFDFLIGVLIFATIVGNVGSMISNMNATRAEFQAKIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        394 VKHYMQFRKVSKDMEAKVIKWFDYLWINKKTVDEREVLKNLPAKLRAEIAINVHLSTLKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       514 LLSAGSCFGEISILNIKGSKMGNRRTANIRSLGYSDLFCLSKDDLMEAVTEAPDAKKVLE
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                  154 LYNWCLLVARACFSDLQRNYFVVWLVLDYFSDTVYIADLIIRLRIGFLEQGLLVKDPKKL
                                                                                                                                                                                                                       122 FYNWCLLVCRACFDELQSEHLTLWLVLDYSADALYVVDMLVRARTGFLEQGLMVRDTKRL
                                      PQSVAADDDTSPELQRLAEMDTPRRGRGGFQRIVRLVGVIRDWANKNFREEEPRPDSFLE
Gaps
27;
  Indels
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Cyclic mucleotide-gated channel 2b.
Rattus norvegicus (Rat).
  94; Mismatches 103;
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MEDLINE=97426406; PubMed=9278419;
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Best Local (
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Matches
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Q9N0H4
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DT 01-00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IGRGVDTWVYPNITDPEYGYLAREXIYCLYWSTLTLTTIGETPPPVKDEFYLFVIFDFLI 361
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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                                                                                                                                                                           76420 MW; 65203ADE66F85F62 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                61.6%; Score 2140; DB 11;
67.0%; Pred. No. 4.8e-150;
iive 88; Mismatches 93;
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InterPro; IPR005821; Ion trans.
InterPro; IPR001622; K-tchannel pore.
Pfam; PF00027; CNMP binding; 1.
Pfam; PF00520; ion trans; 1.
PROSITE; P800809; CNMP; 1.
PROSITE; P800889; CNMP BINDING; 1.
PROSITE; P800889; CNMP BINDING; 1.
Ionic channel; Transmembrane.
SEQUENCE 670 AA; 76420 NW; 65203AD]
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                                                                                                                                                                                                                                    Similarity
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      485 RKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSKMGNRRTANIRS 544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTKKKFELFVLDPAGDWYYRWLFVIAMPVLYNWCLLVARACFSDLQRNYFVVWLVLDYFS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73
Misaka T., Kusakabe Y., Emori Y., Gonoi T., Arai S., Abe K.,
Misaka T., Kusakabe Y., Emori Y., Gonoi T., Arai S., Abe K.,
Taste buds have a cyclic nucleotide-activated channel, CNGgust.";
U. J. Biol. Chem. 272:22523-22529 (1997).
EMBL, AB002801; BAA24353.1;
GO, GO:000521; C:integral to membrane; IEA.
R GO, GO:0005267; F:ion channel activity; IEA.
R GO; GO:0005267; F:ion channel activity; IEA.
R GO; GO:0005267; F:ion transport; IEA.
R GO; GO:0006811; P:ion transport; IEA.
R GO; GO:0006811; P:ion transport; IEA.
R GO; GO:0006811; P:ion transport; IEA.
R GO; GO:0006811; F:ion transport; IEA.
R FO; GO:0006811; Ion Frans.
R InterPro; IPR000595; cNNP binding.
R InterPro; IRR000505; cNNP binding.
R Fam; PF00027; cNNP binding; 1.
R FAMRT; SM00100; cNNP 1.
R RROSITE; PS00889; CNNP BINDING 1; 1.
R RROSITE; PS00889; CNNP BINDING 2; 1.
R RROSITE; PS00889; CNNP BINDING 3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 GRKK--DPIVVDDSSNIYYRWLTAIALPVFYNWCLLVCRACFDELQSEHLTLWLVLDYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIVRLVGVIRDWANKNFREEEPRPDSFLERFRGPELQTVTTHQGDDKGGKDGE-----GK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIVYIADLIIRLRIGELEQGLLVKDPKKLRDNYIHTLOFKLDVASIIPTDLIYFAVGIHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEVRENRILLHFARMFEFFDRIETRISYPNIFRISNLVLYILVLIHWNACIYYVISKSIGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVDTWVYPNITDPEYGYLAREYIYCLYWSTLTLTTIGETPPPVKDEEYLFVIFDFLIGVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IFATIVGNVGSMISNMNATRAEFQAKIDAVKHYMQFRKVSKDMEAKVIKWFDYLWTNKKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        70399 MW; 9ACECEF9EEF63AC4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.4%; Score 2132; DB 11;
67.0%; Pred. No. 1.6e-149;
iive 88; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ą.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Ionic channel; Transmembrane.
SEQUENCE 611 AA; 70399 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   402; Conservative
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PNITOPEYGYLAREXIYCLYWSTLTLTTIGETPPPVKDEEYLFVIFDFLIGVLIFATIVG 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 LEVILDPAGDWYYRWIFFVIAMPVLXNWCLLVARACFSDLQRNYFVVWLVLDYFSDTVYIAD 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192 LIIRLRIGFLEQGILVKDPKKLRDNYIHTLQFKLDVASIIPTDLIYFAVGIHSPEVRFNR 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLHFARMFEFFDRTETRISYPNIFRISNLVLYILVIIHWNACIYYVISKSIGFGVDTWVY 311
82 ANKNFREEEPRPDSFLER-----FRGPELQTVTTHQGDDKGGKDGEGKGTKKKFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 PPSIKANGKODHRAGSRPQSVAADDDTSPELQRLAEMDTPRRGRGGFQRIVRLVGVIRDW
                                                                  597 VDVQEKLEQLETNMDTLYTRFARLLAEYTGAQQKLKQRITVLETKMKQNHEDDYLS 652
                                                                                                                                                                                                                                                                                                                                                                                     Matthews G.; the cyclic nucleotide-gated channel
                                                                                                                                                                                                                                                                        Vertebrata; Euteleostomi;
Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPTFHLEGVD-----QVAMATED-----IIEKKHPDDG----
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PROSITE; PS00889; CNMP BINDING 1; 1.
PROSITE; PS00889; CNMP BINDING 2; 1.
SEQUENCE 637 AA; 73994 MW; 526FIFI16ASDSCFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AVICATA3; AAOLGGOL1; --
GO; GO: GO: GO: C: membrane; IEA.
GO; GO: 0005210; C: membrane; IEA.
GO; GO: 0005217; F: potassium channel activity; IEA.
GO; GO: 0005267; F: potassium channel activity; IEA.
GO; GO: 0006811; P: pot transport; IEA.
GO; GO: 0006811; P: pot transport; IEA.
GO; GO: INFRO0585; CNWP binding.
InterPro; IPRO0585; CNWP binding.
InterPro; IPRO05821; IOn trans.
InterPro; IPRO05821; Ion trans.
FAm; PF00520; CNWP binding; 1.
Pfam; PF00520; CNWP binding; 1.
                                                                                                                                                                                          01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cyclic nucleotide gated channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.5%; Score 1927; DB 13;
59.7%; Pred. No. 2.8e-134;
iive 92; Mismatches 123;
                                                                                                                                                                                                                                                             Bukaryota, Metazoa; Chordata; Craniata;
Actimopterygii, Neopterygii, Teleostei;
Cyprinidae; Carassius.
                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Retina;
Henry D., Burke S., Shishido E.,
"Retinal bipolar neurons express
                                                                                                                                                                                                                                                                                                                                                                                                                      of cone photoreceptors."; J. Neurophysiol. 0:0-0(2003).
                                                                                                                                                                                                                                                         (Goldfish)
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                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Matches 377;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 LILDYVSDIVYLIDMFVRTRIGYLEQGLLVKEELKLINKYKSNLQFKLDVLSLIPTDLLY 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWSTLTLTTIGETPPPVKDEEYLFVIF 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LWINKKTVDEREVLKNLPAKLRAEIAINVHLSTLKKVRIFQDWEAGLLVELVLKLRPQVF 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   538 RTANIRSLGYSDLFCLSKDDLMEAVTEAPDAKKVLEERGREILMKMGLLDENEV-AASME 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 VRLVGVIR-------DWANKNFREEEPRPDSFLERFRGPELQTVTTHQGDDKG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FAVGIHSPEVRFNRLLHFARMFEFFDRTETRTSYPNIFRISNLVLYILVIIHWNACIYYV 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LWTNKKTVDEKEVLKYLPDKLRAEIAINVHLDTIKKVRIFADCEAGLLVELVLKLQPQVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPGDYICKKGDIGREMYIIKEGKLAVVADDGVTQFVVLSDGSYFGEISILNIKGSKAGNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DFLIGVLIFATIVGNVGSMISNMNATRAEFQAKIDAVKHYMQFRKVSKDMEAKVIKWFDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPGDYICRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSKMGNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVLDYFSDTVYIADLIIRLRIGFLEQGLLVKDPKKLRDNYIHTLQFKLDVASIIPTDLIY
                                                                                                                                                            Ratcliffe C.F., Brammar W.J., Conley E.C.;

Ratcliffe C.F., Brammar W.J., Conley E.C.;

"Cloning of cDNAs Encoding cGMP-Gated Cation Channels from Intact
Coronary Arteries and Human Vascular Endothelial Cells.";

Coronary Arteries and Human Vascular Endothelial Cells.";

Submitted (JAN-1997) to the EMBL/Genbank/DDBJ databases.

R GO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:001621; F:ion channel activity; IEA.

R GO; GO:0005267; F:porassium channel activity; IEA.

R GO; GO:0006811; P:ion transport; IEA.

R GO; GO:0006811; P:ion transport; IEA.

R GO; GO:0006811; P:ion transport; IEA.

R InterPro; IPR00595; CNMP binding.

R InterPro; IPR005921; Ion_trans.

R Pfam; PF00027; CNMP binding; 1.

R Pfam; PF00027; CNMP binding; 1.

R SMART; SM00100; CNMP; 1.
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                                                                                   Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 PSIKANGKDDHRAGSRPQSVAADDDTSPELQRLAEMDTPRRGRGGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79125 MW; DB86A7C16CE79D3F CRC64;
                                                                    Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae;
      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.6%; Score 2035; DB 6; 61.4%; Pred. No. 3.1e-142;
                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00888; CNMP BINDING 1; 1. PROSITE; PS00889; CNMP BINDING 2; 1. PROSITE; PS50042; CNMP BINDING 3; 1. Ionic channel; Transmembrane. SEQUENCE 686 AA; 79125 WW; DB86A
      01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   403; Conservative
                                      cGMP-gated cation channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                   [1]
SEQUENCE FROM N.A.
                                                                                                                    NCBI_TaxID=9823;
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Length 637; Indels 81 40 131

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291 KILDKYRQTAQFKWDVISMIPTDLLFIKVGINNPELRINRLTKWMRLFEYFDRTETRTSF 350
                                                             ::|
171 EEEKEEKKEEEPKKEEPKKEEPKKEEKKKEEPPKEIWIMDPSADKYYTWLTIAA 230
                       FELFVLDPAGDWYYRWLFVIAM 151
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Yao H., Vosshall L.B., Tibbs G.R., Sun Z.-P., Young E.C.,

Yao H., Vosshall L.B., Tibbs G.R., Sun Z.-P., Young E.C.,

As Siegelbaum S.A.,

The siegelbaum S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             392 DAVKHYMQFRKVSKDMEAKVIKWFDYLWTNKKTVDEREVLKNLPAKLRAEIAINVHLSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YALLSAGSCFGEISILMIKGSKMGNRRTANIRSLGYSDLFCLSKDDLMEAVTEAPDAKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   591 WCVLSDGAYFGEISILGIKGSKAGNRRTANIRSVGYSDLFALSKDDLMEALTEYPEAKKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEERGREILMKMGLLDENEVAASME-VDVQEKLEQLETNMDTLYTRFARLLAEYTGAQQK
                                                                                                                                                  PVLYNWCLLVARACFSDLQRNYFVVWLVLDYFSDTVYIADLIIRLRIGFLEQGLLVKDPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKVRIFQDWEAGLIVELVLKLRPQVFSPGDYICRKGDIGKEMYIIKEGKLAVVADDGVTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                       351 PIFSESATWYFYILIIIHWNACIFFAIFKIIGFGSDTWVYPTSVTLSTAAFPGSIIYCLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  332 WSTLTLTTIGETPPPVKDEEYLFVIFDFLIGVLIFATIVGNVGSMISNMNATRAEFQAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           272 PNIFRISNLVLYILVIIHWNACIYYVISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
Ictaluridae; Ictalurus.
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Cyclic nucleotide-gated channel modulatory subunit CNGA4a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         609 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     631 LKQRITVLETKMKQNHEDD 649
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                              126 TKKK-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 PDRVRKRNQVGQMPLAMYNMNNCNNTDDKKDDKKDEIKKBEKKQEAQGDEKKEBEKEBEKE 170
                                                                                                                                                               CLSKDDLMEAVTEAPDAKKVLEERGREILMKWGLLDENEVAASMEVDV-QEKLEQLETNM 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65
431
                              KNLPAKLRAEIAINVHLSTLKKVRIFQDWEAGLLVELVLKLRPQVFSPGDYICRKGDIGK 491
                                                                                                                                                                                                                                                        551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QSYPATTROR--PSLCTPNDNLDSIENGTPRSNSECEDTSSEIQGAVSVLTSRHPEPHRD
                                                                                                                                                                                                                                                                                                                                                                                                                               CLSKDDLMEALTEYLDAKAMLEEKGRQILMKDNLLDLELAKQGPDPKVMEEKVIKIGSVL
                                                                                                                                                                                                                                                        EMYLIKEGYLAVVADDGVTQYALLSAGSCFGEISILNIKGSKMGNRRTANIRSLGYSDLF
                                                                                                                                                                                                                                                                                             EMYIIKEGKLAVVADDGVTQFVVLSDGSYFGEISILNIKGSRAGNRTANIRSIGYSDLF
   NVGSMISNMNATRAEFQAKIDAVKHYMQFRKVSKDMEAKVIKWFDYLWTNKKTVDEREVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Decressac S., Grechez-Cassiau A., Lenfant J., Falcon J., Bois P.; Prinary Structure and functional dharacterization of a cGMP gated channel from trout pineal photoeceptor cells "; submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Euteleostei, Protacanthopterygii, Salmoniformes, Salmonidae, Oncorhynchus. VCBI_TaxID=8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---GRGGFQRIVRLVGVIRDWANKNFREEEPRPDSFLERFRGPELQTVTTH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 737;
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SEQUENCE 737 AA; 84900 MW; B2F4B98C51A275CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF39383; ABL59140.1; -
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:000526; F:ion channel activity; IEA.
GO; GO:000526; F:ion channel activity; IEA.
GO; GO:000561; F:potassium channel activity; IEA.
GO; GO:0006811; P:ion transport; IEA.
GO; GO:0006813; P:potassium ion transport; IEA.
InterPro; IPR001595; CMP binding.
InterPro; IPR00152; K-channel pore.
Pfam; PF0027; CMP binding; 1.
Pfam; PF00250; ion trans; 1.
SMART; SM00100; cNMP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53.6%; Score 1862; DB 13;
51.3%; Pred. No. 2.3e-129;
iive 93; Mismatches 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DILYTRFARLLAEYTGAQQKLKQRITVLETKM 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              581 ÓDLOTRFÁRLLÁEHEAAQGKLKKRITKLEKKI 612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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Best Local
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QBUVT8
AC QBUVT8
AC QBUVT8
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DT 01-JUN-
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SEQUENCE FROM N.A.
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Best Local S:
Matches 251
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Q8IV77
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                                                                                                                                                                                                                                                                                                                                                                                                                          313 INKALHNRVNTWYQHLHINKKITRENEILQQLEVTLQTAIAVSVHLPILSKVTIFQNCES 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  432
                                                                                                                                                            TTHOGDDKGGK-DGEGKGTKKK----FELFVLDPAGDWYYRWLFVIAMPVLYNWCLLVA 162
                                                                                                                                                                                                             222
                                                                                                                                                                                                                          282
                                                                                                                                                                                                                                                                             193 LIFILIHWNACLYFALSKYIGLGSDDWYYPDTTDIEFNSTRRQYFYSFWFSTLILTTVGD 252
                                                                                                                                                                                                                                                                                                                                                           TPPPVKDEEYLFVIFDFLIGVLIFATIVGNVGSMISNMNATRAEFQAKIDAVKHYMQFRK 402
                                                                                                                                                                                                                                                                                                                                                                                                            VSKDMEAKVIKWFDYLWTNKKTVDEREVLKNLPAKLRAEIAINVHLSTLKKVRIFQDWEA 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLLVELVLKLRPQVFSPGDYICRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFG 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EISILNIKGSKMGNRRTANIRSLGYSDLFCLSKDDLMEAVTEAPDAKKVLEERGREILMK 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EISILNIKGNKKGNRRTANIRSIGYSDLFSLSKEDLIDTLSEFPAAKRLLEEKGRQILTK 492
                                                                                                                                                                                   72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        639
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                                                                                                                                                                           TOKDGEAQVAKAAEGQKEATKEQKIKVNWREWVIDPSEEFYYGWLQVWVFPIIYNWVVIIL
                                                                                                                                                                                                           RACFSDLQRNYFVVWLVLDYFSDTVYIADLIJRLRIGFLEQGLLVKDPKKLRDNYIHTLQ
                                                                                                                                                                                                                                                            FKLDVASIIPTDLIYFAVGIHSPEVRFNRLLHFARMFEFFDRTETRISYPNIFRISNLVL
                                                                                                                                                                                                                                                                                                             YILVIIHWNACIYYVISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWSTLTLTTIGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UDM-2003 (TrEMBLrel. 24, Last annotation update)
Cyclic mucleotide-gated channel modulatory subunit CNGA4b truncated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     catfish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
Ictaluridae; Ictalurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGLLDENEVAASMEVDVQEKLEQLETNMDTLYTRFARLLAEYTGAQQKLKQRITVLE
                                                                                                                                      9
                                                                                                             cch 41.2%; Score 1433; DB 13; Length 609; al Similarity 49.3%; Pred. No. 1.2e-97; 265; Conservative 121; Mismatches 145; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Siegelbaum S.A.; "Modulatory subunit of cyclic nucleotide-gated channel from olfactory epithelium."; olfactory epithelium."; submitted (UUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Olfactory neuroepithelium;
Yao H., Vosshall L.B., Tibbs G.R., Sun Z.-P., Young E.C.
                                                                                     70313 MW; 5C01AE4B3AB64D24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               551 AA
Pfam; PF00027; cNMP binding; 1.
Pfam; PF00520; ion trans; 1.
SMARY; SM00100; cNMP; 1.
PROSITE; PS00808; CNMP BINDING 1; 1.
PROSITE; PS00809; CNMP BINDING 2; 1.
PROSITE; PS0042; CNMP BINDING 2; 1.
Ionic channel; Transmembrane.
SEQUENCE 609 AA; 70313 MW; 5C01AE41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 PILSKVTIFQNCESSLLEELVLKLTPQVXNPGEYVCRKGDVGHEMYIIKEGKLAVVADDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149 IAMPVLYNWCLLVARACFSDLQRNYFVVWLVLDYFSDTVYIADLIIRLRIGFLEQGLLVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  209 DPKKLRDNYIHTLQFKLDVASIIPTDLIYFAVGIHSPEVRFNRLLHFARMFEFFDRTETR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269 TSYPNIFRISNLVLYILVIIHWNACIYYVISKSIGFGVDTWVYPNITDPEYGYLAREYIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKIDAVKHYMQFRKVSKDMEAKVIKWFDYLWTNKKTVDEREVLKNLPAKLRAEIAINVHL
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
5imilar to cyclic uncleotide gated cation channel (Fragment)
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                   Ionic channel; Transmembrane.
SEQUENCE 551 AA; 63371 MW; 8C51F06B88545B0D CRC64;
EMBLY RESEARCH CONTROLL OF GRANDERS I EAR.

(GO; GO: 0016021; C:integral to membrane; IEA.

(GO; GO: 0005216; F:ion channel activity; IEA.

(GO; GO: 0006811; P:ion transport; IEA.

(GO; GO: 0006813; P:ion transport; IEA.

(GO; GO: 0006813; P:ion transport; IEA.

(InterPro; IPRO0555; CMP_binding.

(InterPro; IPRO0525; K+channel_pore.

(Fam; PF00027; CMP_binding; 1.

(R SMART; SW00100; CMP; 1.

(R PROSITE; PS00889; CMMP_BINDING_1; 1.

(R PROSITE; PS00889; CMMP_BINDING_2; 1.

(R PROSITE; PS00889; CMMP_BINDING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 39.6%; Score 1375; DB 13;
11 Similarity 51.1%; Pred. No. 2.1e-93;
251; Conservative 108; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       474 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               377 ISNMNATRAEFQAKIDAVKHYMQFRKVSKDMEAKVIKWFDYLWTNKKTVDEREVLKNLPA 436
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                                                                                          511 QYALLSAGSCFGEISILNIKGSKMGNRRTANIRSLGYSDLFCLSKDDLMEAVTEAPDAKK 570
  LKKVRIFQDWEAGLLVELVLKLRPQVFSPGDYICRKGDIGKEMYIIKEGKLAVVADDGVT 510
                                                                                                                    2 PEYGRLSRKYIYSLYWSTLTLTTIGETPPPVKDEFYLFVVIDFLVGVLIFATIVGNYGSM 61
                         LKRVEIFONTEAGFLCELVLRLRPVLFSPGDYICRKGEVGKEMYIVNRGRLOVVADNGKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi; Muridae, Murinae, Rattus,
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Qiu W., Guggino S.E.;
"Cyclic nucleotide-gated cation channel (CNG3) expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tidney.";
Submitted (CCT-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; ARDS1944; AABR065.1;
R GO; GO:0016020; C:membrane; IEA.
GO; GO:0005267; F:potassium channel activity; IEA.
GO; GO:0006813; P:potassium ion transport; IEA.
GO; GO:0006813; P:potassium ion transport; IEA.
R InterPro; IPR001652; K+chānnel_pore.
R InterPro; IPR001655; CMPP binding.
Fram; PF00027; CMPP binding; 1.
PROSITE; PS000888; CMMP_BINDING_1; 1.
PROSITE; PS00888; CMMP_BINDING_2; 1.
PROSITE; PSS0042; CMMP_BINDING_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUV-2003 (TrEMBLrel. 24, Last annotation update)
Cyclic nucleotide-gated cation channel (Fragment).
CMG3.
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242 DLMETLTEYPE 252
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252 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               395 YDYSWSRGRIQGGGDINTALGLLPDKLKTELALHVNLSVLKKVTIFQECQPEFLHDLVLK 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         295 YYVISKSIGFGVDTWVYPNIIDPEYGYLARBYIYCLYWSTLTLTTIGETPPPVKDEEYLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 VVWLVLDYFSDTVYIADLIIRLRTGFLEQGLLVKDPKKLRDNYIHTLQFKLDVASIIFTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                355 VIEDFLIGVLIFATIVGNVGSMISNMNATRAEFQAKIDAVKHYMQFRKVSKDMBAKVIKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FDYLWINKKIV---DEREVLKNIPAKIRAEIAINVHISTIKKVRIFQDWEAGLLVELVLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRPQVFSPGDYICRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82; Gaps
                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta, Pterygota,
Bobytera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 30.7%; Score 1068; DB 5; Length 1463; Best Local Similarity 35.6%; Pred. No. 5.2e-70; Matches 234; Conservative 136; Mismatches 206; Indels 82,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Miyazu M., Tanimura T.;

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                                                                             C1-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UJV-2003 (TrEMBLrel. 24, Last annotation update)
CNG channel-like.
CNG CAG9176.
    1463 AA
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218
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636 T-----NTPEPTAA 663
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